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The invention relates to methods for the screening, diagnosis and prognosis of Alzheimer's disease. The methods involve the detection of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or Expression Reference Protein Isoform (BRPI) in order to determine whether a patient is suffering from, or has a predisposition to, Alzheimer's Disease. The relative abundance of the AFs and APIs correlates with the severity of Alzheimer's Diseases. The present sequence is a peptide
                                                                                                                                                                                                                                                                                                                                        Screening for Alzheimer's disease in a mammal, by making two-dimensional array of a feature whose relative abundance correlates with disease, and comparing with abundance of the feature in samples of healthy persons.
                                                                                                                                                                                                                   Durham KL, Friedman DL, Herath HMAC, Kimmel LH, Parekh RB;
Potter DM, Rohlff C, Silber BM, Stiger TR, Sunderland PT;
Townsend RR, White F, Williams SA;
                                                                                                                                                         (OXFO-) OXFORD GLYCOSCIENCES UK LTD. (PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                          Example, Page 30; 162pp; English.
                                                                                               03-APR-2000; 2000US-0194504P.
28-NOV-2000; 2000US-0253647P.
                                                        03-APR-2001; 2001WO-US010908.
                                                                                                                                                                                                                                                                                                   WPI; 2001-639384/73.
                   11-OCT-2001.
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6 Query Match 60.6%; Score 20; DB 4; Length 7; Best Local Similarity 57.1%; Pred. No. 1.4e+06; Matches 4; Conservative 1; Mismatches 2; Indels Sequence 7 AA;

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1 FTLKISR 7 || : || 1 FTFEYSR 7 g ઠ

Search completed: June 1, 2004, 11:16:18 Job time : 47.6667 secs

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The invention relates to methods and compositions for screening, the invention relates to methods and compositions for screening, the diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) in samples, e.g. by electrophoresis, associated Protein Isoforms (SFIS) in samples, e.g. by electrophoresis, inmunoassay or hybridisation assay, for diagnosing and monitoring SCH, studying the effectiveness of treatments and for identifying potential control of the relative abundance of at least 1 chosen feature correlates (SCH) and the relative abundance of at least 1 chosen feature which correlates with the presence or absence of SCH; and (2) monitoring the effect of the charpy administered to a subject with SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The secondary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectiveness of treatment and as targets to dentify and produce potential therapeutic agents for the treatment of SCH. The paucity of detectable neuralgic defects distinguishes neuropsychiatric disorders such as SCH from neurological disorders, where many cases. Consequently the identification and characterisation of necessary for improve direatment of neuropsychiatric disorders and neuropsychiatric disorders. ANUISTR cellular and/or molecular causative defects and neuropsychiatric disorders. ANUISTR sepresent the anino acid sequences of schizophrenia-associated is seferited.
                                                                                                                                                                                                                                                                                                                                                                       Diagnosing and monitoring Schizophrenia by detecting the presence of Schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid.
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Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
Expression Reference Procein Isoform; ERPI; proteolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 42.9%; Score 20; DB 4; Length 7; Similarity 42.9%; Pred. No. 1.4e+06; 3; Conservative 3; Mismatches 1; Indels
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                                                                                                                                                                                                           (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                 Rohlff C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 32; 160pp; English.
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                                                                               23-FEB-2001; 2001WO-GB000783,
                                                                                                                               24-FEB-2000; 2000GB-00004415
28-DEC-2000; 2000US-00750395
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Best Local Similarity
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1 YTFELSR 7
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a preparation comprising an isolated Bipolar Affected Disorder (BAD)-Associated Protein Isoform (DPIS). The DPI's are used to screen, diagnose or tryognose of BAD or unipolar depression, identify a determine the stage or severity of BAD or unipolar depression, identify a subject at risk of developing BAD or unipolar depression, or monitor the effect of therapy in a subject. They are also used to screen for or identify agents that interact with a DPI. These agents, antibodies against the DPIs, and mucleic acids encoding the DPIs are used to treat or prevent BAD or unipolar depression. Diseases that can be treated are attention deficient disorder, a schizoaffective disorder, a bipolar or a minjolar affective disorder. The DPIs are used in proteomics. The proteomic approach of using DPIs for screening, diagnosis of proteomic approach of using DPIs for screening of using gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression analysis, such as not being able to obtain central nervous system (CNS) tissue from a living patient under normal circumstances. The present sequence is a DIP decreased in the CSF (cerebro-spinal fluid) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preparation for diagnosing or treating bipolar affected disorder (BAD) unipolar depression, or for screening for modulators, comprises a BAD-associated protein isoform.
CSF; antidepreBsant; antimanic; nootropic; tranquiliser; neuroleptic; attention deficient disorder; schizoaffective disorder; unipolar affective disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                            (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herath HMAC, Parekh RB, Rohlff C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Page 34; 163pp; English.
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08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
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Query Match
Best Local Similarity 42.9°,
Bernes 3; Conservative
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1 YTFELSR 7
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                                                                                                        Homo sapiens.
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RESULT 14 AAU15313

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1 YTFELSR 7
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                                                                                                              AAU24969;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest deptides of these proteins. Some of the DPIs (AAU28404-AAU28625) described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar affective disorder) ambjects, whilst other DPIs (AAU28626-AAU28887) are increased in BAD subjects, Also described are peptide sequences identified from DPI-45 and DPI-31 and the nucleic acid sequence they are encoded by. The sequences of the invention are useful for clinical screening, diagnosis, prognosis, therapy and prophylaxis of meuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder, schizoaffective disorders, and unipolar affective disorders. The present sequence represents one of the DPI tryptic diseates. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.
                                                                                                                                                                                                                                                                                        Human; depression associated protein isoform; tryptic digest peptide; DPI; cerebrospinal fluid; CSF; BAD; bipOlar affective disorder; neuropsychiatric disorder; bipolar mood disorder; neuroleptic; maniac-depressive illness; schizoaffective disorder.
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                                               Score 20; DB 4; Length 7; Pred. No. 1.4e+06; 3; Mismatches 1; Indels
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treatment of VD and for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 34; 153pp; English.
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                                                                                                                                                                                       AAU28602 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                 DPI tryptic digest peptide #199.
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08-DEC-2000; 2000GB-0030050.
12-DEC-2000; 2000US-0254830P.
                                               60.68;
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Best Local Similarity 42.9
Matches 3; Conservative
                                                                          3; Conservative
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AAU28602
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New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
                                                                                                                                                                                                                                        Schizophrenia-associated protein isoform, SPI, SPI-206, SPI-238, SPI-240, neuroleptic, gene therapy, cerebrospinal fluid, serum, plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs
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                                                                                                                                                                           Schizophrenia-Associated Protein Isoform (SPI) peptide #198.
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AAU24969 standard; peptide; 7 AA
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28-DEC-2000; 2000US-00750395.
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Best Local Similarity 42.3%,
Annes 3; Conservative
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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VDI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VD-associated protein isoform; VPI; screening;
comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
                                                                                                                                                                                                                                                                                                                                                                               Query Match 60.6%; Score 20; DB 4; Length 7; Best Local Similarity 42.9%; Pred. No. 1.4e+06; Matches 3; Conservative 3; Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vascular dementia-associated protein isoform (VPI) 483.
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                                                  Claim 6; Page 31; 151pp; English.
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24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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1 YTFELSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dementia;
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                                                                                                                                                                                                                                                                                                                                                Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vascular
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ABB56283
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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance

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Gaps

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correlates with the presence, absence, stage or severity of VD or perdicts the onset or course of VD. especially detecting in a sample of cerebrosphial fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABBSS801-ABBS5295) as fully defined in the protein isoforms (VPIS) (ABBSS801-ABBS5295) as fully defined in the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of erebrospinal fluid (CSF) from the subject one of 23 VD associated protein isoforms (VPIS) (ABBS5091-ABBS5295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the
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                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein isoform; VPI; screening;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening, diagnosis or prognosis of vascular dementia (VD), useful determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
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                                                                                                                                                                                                                                                        Score 20; DB 4; Length 7;
Pred. No. 1.4e+06;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vascular dementia-associated protein isoform (VPI) 181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vascular Dementia, VD; VD-associated diagnosis; prognosis; gene therapy.
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                                                                                                                                                                                                                                                        60.6%;
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24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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                                                                                                                                                                                                                                                                                                  3; Conservative
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                        1 FTLKISR 7
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                                                                                                                                                                                                                     Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB55981;
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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Peptides AAR81847-54 are tryptic peptide fragments from human afamin (AAR81845) novel member of the human serum protein family. The fragments were used to design primers and probes (AAT00786-98) for the cloning of the afamin gene (AAT00785) from human liver cDNA. Afamin is thought to have similar properties to human albumin, alpha-foetoprotein and vitamin be binding protein due to homology with these proteins. The gene encodes a mature protein of 66576 daltons without post-translational processing (ca. 87000 daltons with post-translational processing). The protein was protein can be used to ameliorate ischemia-reperfusion injury, protein can be used to ameliorate ischemia-reperfusion injury, rheumatcid arthritis, ARDS, cardiopulmonary bypass, sepsis, toxic plasma substances released after inflammation, etc
                                                                                                                                                                  Human afamin or a variant and poly:nucleotide(s) encoding it - a human serum protein with activities in common with other members of this family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection; rheumatoid arthritis diagnostic feature; BRDI; synovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
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                                                                                                                         Wright SD;
                                                                                                                       Wurfel MM,
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                                                                                                                                                                                                                                                  Example 3; Page 45; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY41889 standard; peptide; 7 AA.
                31-MAR-1995; 95WO-US004075.
                                            94US-00222619
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                                                                                                                       Lichenstein HS, Lyons DE,
                                                                          AMGEN INC.
UNIV ROCKEFELLER.
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                                                                                                                                                       WPI; 1995-358634/46.
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FTFEYSR '
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                                              31-MAR-1994;
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(UYRQ )
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arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comparises: (a) analysing a sample of serum or plasma and optionally comparises: (a) analysing a sample of serum or plasma and optionally comparises: (b) identifying at least one chosen dimensional array of features; (b) identifying at least one chosen cature whose relative abundance correlates with the presence or absence of RA, and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in serum or plasma from or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical attudies for testing drugs for therapy of RA, for purification of RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to AAX25066 to AAZ25068 represent dependence protein isoform peptides and AAZ25066 to AAZ25068 represent dependence protein isoform peptides and can be used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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human rheumatoid arthritis by two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.6%; Score 20; DB 2; Length 7; Best Local Similarity 42.9%; Pred. No. 1.4e+06; Matches 3; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vascular dementia-associated protein isoform (VPI) 70.
                                                         Disclosure; Page 18; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OXFO-) OXFORD GLYCOSCIENCES UK LID.
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24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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1 YTFELSR 7
                   electrophoresis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7 AA;
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arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally comprises: (a) analysing a sample of serum or plasma and optionally comprises: (a) analysing a sample of serum or plasma and optionally comprises: (b) identifying at least one chosen dimensional array of features; (b) identifying at least one chosen feature whose relative abundance corraltes with the presence or absence of RA, and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in the sample with the abundance of the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy protected a AAX1844 to AAX2100 represent RPI peptides, AAX42101 to AAX225066 to AAX225068 represent descent invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; afamin; serum protein family; albumin; alpha-foetoprotein; plasma; vitamin D binding protein; homology; post-translational processing; thromatography; Primar; PRR, amplification; probe; rheumaroid arthritis; ischaemia-reperfusion injury; ARDS; cardiopulmonary bypass; sepsis; toxic plasma substance; inflammation.
                                                                                                                                                                                                                                                                       Diagnosis of human rheumatoid arthritis by two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 63.6%; Score 21; DB 2; Length 7; Best Local Similarity 83.3%; Pred. No. 1.4e+06; Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                     (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 21; 157pp; English.
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                                                                                                                                                                                 Parekh RB, Patel TP,
                                                                                                                                                                                                                              WPI; 1999-571871/48.
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                                                                                                                                                                                                                                                                                                   electrophoresis.
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                                            15-MAR-1999;
                                                                                        13-MAR-1998;
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23-SEP-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention is concerned with producing scaffold proteins based upon the human CTRA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthitis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
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                                                                                                                                                                                                  Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
diabetic retinopathy; atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rheumatoid arthritis diagnostic protein isoform peptide #164.
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                                                                                                                                                        Scaffold protein SCA S4 peptide SEQ ID NO: 137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Desmet J, Hufton S, Hoogenboom H, Sablon E;
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                 AAB30076 standard; peptide; 7 AA
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                                                                                                                                                                                                                                                                                              Synthetic.
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RESULT 5
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or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold may be bound to a protein which binds to a tumour antigen. This will target the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, CTLA-4; scaffold protein; antigen-binding; receptor-binding;
SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
diabetic retinopathy; atherosclerosis.
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                                                                                                                                                                                                                  Query Match 69.7%; Score 23; DB 2; Length 7; Best Local Similarity 83.3%; Pred. No. 1.4e+06; Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scaffold protein SCA S4 peptide SEQ ID NO: 135.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB30074 standard; peptide; 7 AA.
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                                                                                                                                                                                            Sequence 7 AA;
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New scaffold protein, useful for stabilizing antigens used as vaccines.

Disclosure; Page 6; 105pp; English.

Scaffold protein; beta strand; beta sheet; stabilize antigen; tumour; chemotherapeutic agent. 84 derivative #12, beta strand of scaffold protein structure.

98EP-00870065.

EP947582-A1 06-0CT-1999.

Synthetic.

(INNO-) INNOGENETICS NV.

31-MAR-1998;

AAY40738 standard; peptide; 7 AA.

FTLSIS

01-DEC-1999 (first entry)

AAY40738;

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Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands 12.56, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands functionally equivalent derivative of these sequences. The beta strands formered so the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures of the next by hydrogen bonds, which beta strands are connected to each other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold may be bound to a protein which binds to a tumour antigen. Therefore the scaffold protein may be used to target the complex to tumour cells. Another surface may be bound to a qrotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used in stabilize individual peptides in a peptide library and may be used in clayers.
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Matches 5; Conservative
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Length 7;

Query Match
69.7%; Score 23; DB 3; I
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 1;

1 FTLKIS 6

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Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands s1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands of form two beta sheets $1/$4/$3 and $5/$5/$2 and beta sandwich architecture. If the additional beta strands A1-3 are beta sandwich architecture. If the additional beta strands A1-3 are included in the structure the scaffold is constructed of two beta sheets, with the structures and $5/$5/$2/$2/$2/$3.73 The beta strands are connected to cher via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens
                           Abriotel Human sec
Abbelles4 Staphyloc
Abu69381 Respirate
Abu69381 Respirate
Ade77927 Synthetic
Aaw84431 HIV-1 nuc
Aaw84431 HIV-1 nuc
Aav879594 Microtetr
Aar7797 Antigenic
Aar7797 Antigenic
Aar7797 Antigenic
Aar7797 Synthetic
Ade38847 SYNAGIS a
Ade37847 SYNAGIS a
Ade77919 Synthetic
              Human RSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New scaffold protein, useful for stabilizing antigens used as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 derivative #10, beta strand of scaffold protein structure.
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ADB79629
ABP66518
ABB81854
ABB8185876
ADB77927
AAW84831
AAR877970
AAR97970
AAW69269
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                                                                                                                                                                                                                                                                                                                                                                                                                AAY40736 standard; peptide; 7 AA.
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31-MAR-1998;
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                                                                                            June 1, 2004, 10:40:31; Search time 45.6667 Seconds (without alignments) 43.310 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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AAB30074
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ABB55281
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Gapop 10.0 , Gapext 0.5
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MEDLINE=97351561; PubMed=9207843;
Octiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
Octiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
Octiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;

"Differential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in Buspension cultures of tomato
[Lycopersicon esculentum].";
Plant Mol. Biol. 34:275-286(1997).

EMBL, U75692; AAC49682.1; -.

GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
                      Eukaryota, Viridiplantae; Streetiophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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27.3%; Score 9; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
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27.3%; Score 9; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
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STRAIN-Sprague-Dawley;
Prietto S.M., Lyons J.G.;
submitted S.M., Lyons J.G.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY101357; AAM51172.1; -.
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SEQUENCE 7 AA; 907 MW; 63373B51EB1DD9A0 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
COllagenase-3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        063480 PRELIMINARY, PRT, 7 AA.
03480, 01-NOV-1996 (TEMBLrel. 01, Created)
01-NOV-1996 (TEMBLrel. 01, Last sequence update)
01-UNN-2003 (TEMBLrel. 24, Last annotation update)
TR4-NS orphan receptor (Fragment).
                                                                                                                                                                                                                                                                                       NON TER 1 1 1
SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;
               ycopersicon esculentum (Tomato)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-96199747; PubMed=8612486;
Yoshikawa I., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
Beteara-Wadleigh S.D.;
"Splice variants of rat TR4 orphan receptor: differential expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                 of novel sequences in the 5'-untranslated region and C-terminal
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7 AA; 758 MW; 672AAB7864005350 CRC64;
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EMBL; U59125; AAB02827.1; -.
GO; GO:0004872; F:receptor activity; IEA.
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Stevenson B., Miller J.C.;
"Comparative analyses of Borrelia burgdorferi erp genes and their cp32 prophages: conservation amidst diversity.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY141106; AAN17857.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
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Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                             Borrelia burgdorferi (Lyme disease spirochete).
Plasmid group cp32-13.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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"Isolation of chromosome-specific genes by reciprocal probing of arrayed cosmid libraries.";

Hum. Mol. Genet. 0:0-0(1995).

EMBL; L32077; AAA73887.1;

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SEQÜENCE 7 AA, 814 MW, 672B1DD3372046B0 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
(Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(Clone STSFA1LA) (Fragment).
  24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER 1 1 SEQUENCE 7 AA, 928 MW; 6337233050437350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.3%; Score 9; DB 4
100.0%; Pred. No. 1e+
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 2; Conservative
01-JUN-2003 (TrEMBLrel. 2 PF-50 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=CA15;
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P93233
AD P93233
DT 01-MA
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DE (Fragil
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DE REPRESENTANT PRESENTANT PRESEN
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                                                                                                                                                                                                                                                                                                                               Stevenson B., Miller J.C.;
Stevenson B., Miller J.C.;
"Comparative analyses of Borrelia burgdorferi erp genes and their cp32 prophages: conservation amidst diversity.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX142100; AAN17911.1;
GQ; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=93-0107;
Stevenson B., Miller J.C.;
"Comparative analyses of Borrelia burgdorferi erp genes and their cp32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                Plasmid group cp32-9.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia burgdorferi (Lyme disease spirochete).
Plasmid group cp32-5.
Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Borrelia.
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OBGLO4;

O1-MAR-2003 (TrEMBLrel. 23, Created)

O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)

O1-JUJN-2003 (TrEMBLrel. 24, Last annotation update)

PF-50 protein (Fragment).
                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
PP-50 protein (Fragment).
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SEQUENCE 7 AA; 849 MW; 6337244330569ED0 CRC64;
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(TrEMBLrel. 23, Last sequence update)
                                                                                                                                                      Borrelia burgdorferi (Lyme disease spirochete)
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                   STRAIN=N40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Q8GL00
ID Q8GL0
AC Q8GL0
DT 01-MA
DT 01-MA
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Q8GL04
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STRAIN=RF-1;
WEDLINE=99231861; PubMed=10217509;
Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
"Organization and expression of nitrogen-fixation genes in the aerobic nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
                                                                                                                                                                                                                                                                                             Rattus sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothece PCC 8801)
Bacteria; Cyanobacteria; Chrococcales; Cyanothece.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Gunn;
MEDLINE=91282788; PubMed=1840486;
MEDLINE=91282788; PubMed=1840486;
Sato H., Aono S., Kashiwanta S., Koiwai O.;
Sato H., Aono S., Kashiwanta S., Koiwai O.;
Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";
Biochem. Biophys. Res. Comunn. 177:1161-1164 (1991).
EMBL; S38636; AAB19255.1;
GO, GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.3%; Score 9; DB 11; Length 4; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 2; Conservative 0; Mismatches 0; Indels
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                                                                                                                       008433;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Bilirubin UDP-glucuronosyltransferase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UUL-1997 (TrEMBLrel. 04, Created)
01-UUL-1997 (TrEMBLrel. 04, Last sequence update)
01-UL-1901 (TrEMBLrel. 19, Last annotation update)
N1fK (Fragment).
NIFK.
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SEQUENCE 4 AA, 473 MW; 633732C42000000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA.
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                                                                                                  PRT;
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EMBL; AF003700; AAC35193.1; -.
                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Q8GL12
ID Q8GL12
                                                                                                  Q08433
                               RESULT 7
Q08433
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Chloroplast.

Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; Caryophylales, Amaranthaceae, Spinacia.
                                                                                           STRAIN=D273-10B;
MEDLINE=81069885; PubMed=6254986;
MEDLINE=8.06., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
MAssembly of the mitochondrial membrane system: Structure and
nucleotide sequence of the gene coding for subunit 1 of yeast
cytochrome oxidase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.3%; Score 11; DB 8; Length 7; Best Local Similarity 66.7%; Pred. No. 1e+06; Matches 2; Conservative 1; Mismatches 0; Indels
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 30S ribosomal protein S19 beta (Fragment).
Spinacia oleracea (Spinach).
                                                                                                                                                                                                                                                                                   J. B101. Chem. 255:11927-11941(1980).

EMBL, V00694; CAA24066.1; -.

GO; GO:0005739; C:mitochondrion; IEA.

Mitochondrion.

NOW TER

SEQUENCE 7 AA, 859 MW; 75B7232362CDC460 CRC64;
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                                                           SEQUENCE FROM N.A.
NCBI_TaxID=4932;
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RESULT 6 P82541

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SEQUENCE.

STRAIN=DSM 20451;

PubMed=12112860;

Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;

"High pressure effects step-wise altered protein expression in Dractobacillus anafranciscensis.";

Proteomics 2:765-774 (2002).

-I- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN PROTEIN IS: 15 KDA.
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-01W-2003 (TrEMBLrel. 24, Last annotation update)
11side intron 5 (Fragment).
Saccharomyces cerevisiae (Baker's yeast).
Mitochondrion.
Mitochondrion.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P83530 PRELIMINARY; PRT; 7 AA.
P83530,
01-UTN-2003 (TYEMBLrel. 24, Created)
01-UTN-2003 (TYEMBLrel. 24, Last sequence update)
01-UTN-2003 (TYEMBLrel. 24, Last annotation update)
Unknown protein from 2D-page (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria; Pirmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBI_TAXID=1625;
                                                                                                                                                                                                                                                                                                                Query Match 36.4%; Score 12; DB 5; Length 7; Best Local Similarity 66.7%; Pred. No. 1e+06; Matches 2; Conservative 1; Mismatches 0; Indels
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33.3%; Score 11; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 1; Indels
                                                                                                                                                             SEQUENCE FROM N.A.
STRAINE-Bristol N2;
Wilson R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AR043704; AA038892.1; -.
Hypothetical protein.
SEQUENCE 7 AA, 874 MW; 72DIA9DB5041A6F0 CRC64;
Bradshaw H., Graves T., Blair T.;
"The sequence of C. elegans cosmid W01B11.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                           Waterston R.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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NON_TER 7 7
SEQÜENCE 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;
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                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
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TLDV 5
                                                                                                                                                                                                                                                                                                                                                                                    1 FTL 3
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5 FTV 7
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P83530
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AC Q9599, AC Q9599, DT 01-FI
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                       P82182, PRELIMINARY, PRT, 6 AA.

92182, 92182, 92182, 92182, 01-070-2000 (TrEMBLrel. 14, Created)
01-070-2000 (TrEMBLrel. 14, Last sequence update)
01-070-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 50S thosomal protein L10 gamma (Fragment).
Spinacia oleracea (Spinach).
Spinacia oleracea (Spinach).
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophylales; Amaranthaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
39.4%; Score 13; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels
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01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=99069613; PubMed=9851916;
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RESULT 3 Q7Z1C0

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SEQUENCE.

us-09-712-819c-6.closed.rspt

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RESULT 1
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P82182 spinacia ol
O721C0 caenorhabdi
P83530 lactobadill
O95945 saccharomyc
P82541 spinacia ol
Q06433 rattus sp.
O07354 synechococc
O89112 borrelia bu
Q89110 borrelia bu
Q89110 borrelia bu
Q89110 horrelia bu
Q89110 horrelia bu
Q89110 korrelia bu
Q89100 korrelia bu
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1 FTLKISR 7
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## ALIGNMENTS

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-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- STMILARLIY: Belongs to the allatostatin family.
Neuropeptide; Multigene family.
SEQUENCE 7 AA; 782 MW; 672879CDCB476ACO CRC64;
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Bur. J. Biochem. 250:727-734(1997).

-I- FUNCTION: May act as a neurotransmitter or neuromodulator.

-I- SIMILARITY: Belongs to the allatostatin family.

Nouropeptide; Amidation; Multiplene family.

MOD_RES.

7 AMIDATION.

SEQÜENCE 7 AA; 781 MW; 672879CDCB476420 CRC64;
                                                                                   TISSUB-Cerebral ganglion, and Thoracic ganglion;
MEDLINE-98121193; PubMed-9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
TISSUB-Cerebral ganglion, and Thoracic ganglion;
MEDLINE-98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Carcinustatin 5.
Carcinus maenas (Common shore crab) (Green crab).
Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
NUBL TaxID=6759;
Eumalacostraca, Eucarida, Decapoda, Pleocyemata, Brachyura, Eubrachyura, Portunoidea, Portunidae, Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.2%; Score 8; DB 1; Length 7; 66.7%; Pred. No. 1.4e+05; tive 0; Mismatches 1; Indels
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24.2%; Score 8; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indele
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Best Local Similarity 66.7
Matches 2; Conservative
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P81808;
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ALLS CARMA
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Search completed: June 1, 2004, 11:16:49 Job time : 7.66667 secs

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"ISOJATION and identification of multiple neuropeptides of the allacostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide, Amidation, Multigene family.
MOD RES 7 7 MIDATION (POTENTIAL).
SEQUENCE 7 AA, 770 MM; 672879CDGSDDB70 CRC64;
                                                                SEQUENCE.
TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Bumalacostraca; Bucarida; Decapoda; Pleocyemata; Brachyura;
Bubrachyura; Portunoidea; Portunidae; Carcinus.
NCBI_TaxID=6759;
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P81807;
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ALL3 CARMA
ID ALL3 CARN
AC P81806;
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                                                                                                                                                                                                                                                                                                                                       F3CT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-
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-!- SUBCELLAR LOCATION: Secreted.
-!- PTM: Sulfation is important for activity and for the binding to
    putative membrane receptor (By similarity).
-!- SIMILARITY: Belongs to the phytosulfokine family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. US-Harumanicon.

MEDLINE=20212743; PubMed=10750705;

MEDLINE=20212743; PubMed=10750705;

MEDLINE=20212743; PubMed=10750705;

Matsubayashi Y., Kobayashi T.,

Kamada H., Sakagami Y., Yamamoto M., Matsubayashi Y., Kobayashi T.,

"A secreted peptide growth factor, phytosulfokine, acting as a stimulatory factor of carrot somatic embryo formation.";

Plant Cell Physiol. 41:27-32 (2000).

-I- FUNCTION: In presence of 2,4-D, stimulates proliferation of the cells, but does not stimulate differentiation into the somatic
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allatostatin superfamily in the shore crab Carcinus maenas.";

Eur. J. Biochem. 250;727-734 (1997).

-i. FUNCTION: May act as a neurotransmitter or neuromodulator.

-i. SIMILARITY: Belongs to the allatostatin family.

Neuropeptide; Amidation; Multisgene family.

AMOD RES

5 An MAD RES

5 AN S86 MW; 672879D5AB300000 CRC64;
                                                                                                                                                              1; Indels
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Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.2%; Score 8; DB 1; Length 5; 50.0%; Pred. No. 1.4e+05; ative 1; Mismatches 0; Indels
                                                                                                                               24.2%; Score 8; DB 1; Length 5; 66.7%; Pred. No. 1.4e+05; ive 0; Mismatches 1; Indel.
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1 1 SULFATION.

3 3 SULFATION.

5 AA, 687 MW, 76C1BB504B300000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY
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ALL2 CARMA
ID _ALL2 CARMA STANDARD; PRT; 7 AA.
AC    P81805;
DT    30-MAY-2000 (Rel. 39, Last sequence update)
DT    30-MAY-2000 (Rel. 39, Last annotation update)
DT    30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus talin 2.
OS Carcinus maenas (Common shore crab) (Green crab)
OC    Eukaryota; Metazoa; Arthropoda; Crustacea; Malacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth factor; Sulfation.
PEPTIDE 1 4
MOD_RES 1 1
MOD_RES 3 SEQUENCE 5 AA; 687 MW;
                                                                                                                                               Best Local Similarity 66.7
Matches 2; Conservative
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Daucus carota (Carrot)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4039;
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P58261;
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PSK_DAUCA
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MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                Carcinustatin 3.
Carcinus maenas (Common shore crab) (Green crab).
Bukaryota, Metazoa, Arthropoda; Crustacea; Malacostraca;
Bumalacostraca; Bucarida; Decapoda; Pleocyemata; Brachyura;
Bubrachyura; Portunoidea; Portunidae; Carcinus.
                                                     1; Indels
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Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
24.2%; Score 8; DB 1; Length 7; 66.7%; Pred. No. 1.4e+05; tive 0; Mismatches 1; Indels
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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30-MAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
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Gaps

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1; Indels

Pheromone. SEQUENCE

SXACCR

Query Match

Best Loc Matches

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RESULT 7 CHOX ALCSP ID CHOX ALCSP

P16101;

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TISSUE=Coleoptile,

Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,

Pernollet J.-C., Zivy M., de Vienne D.;

"The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome analysis program.";
Theor. Appl. Genet. 93:997-1005 (1996).
-!- MISCELLANSOUS: On the 2D-gel the determined pI of this unknown protein is: 6.0, its MW is: 30.0 kba.
Maize-2DPAGE; P80630; COLEOPTILE.
MaizeDB; 123956; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Uhknown protein from 2D-page of etiolated coleoptile (Spot 447)
(Fragment).
Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
Thorpe A.;
"Isolation and identification of multiple neuropeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carcinus maenas (Common shore crab) (Green crab).
Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleccyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
        -i- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1. PR.; A25269; A25269. Pheromone SEQUENCE 7 Aa; 734 MW; 75BDD72059C05DB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.3%; Score 9; DB 1; Length 7; larity 66.7%; Pred. No. 1.4e+05; Conservative 0; Mismatches 1; Indels
                                                                                                                                                 27.3%; Score 9; DB 1; Length 7; 66.7%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;
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ALI4 CARMA
ID ALI4 CARMA
ID ALI4 CARMA
STANDARD; FRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
Carcinus maenas (Common shore crab) Cos Carcinus meanas (Common shore crab) Cos Carcinus meanas (Common shore crab) Cos Carcinus Euhalacostraca; Eucarida; Decapoda; Plecoyemata;
Cos Euharacytura; Portunoidea; Portunidae; Carcinus.
Cos Carcinus Portunoidea; Portunidae; Carcinus.
Cos MEDILINE-98121193; PubMed-9461295;
Cos MEDILINE-98121193; PubMed-9461295;
Cos Carcinus Carcinus Carcinus A. Houve H., Johnsen A.H., Maestro J.-L., Scott A.G., RA Thorpe A.;
Ilsolation and identification of multiple neurope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Cerebral ganglion, and Thoracic ganglion; MEDLINE-98121193; PubMed-9461295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 A.
                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                         Local Similarity 66.7 es 2; Conservative
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Beet Local Similarity
2, Conserve
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P80630;
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                                                                                                                                                 Query Match
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UC24 MAIZE
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Matches
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01-0cr.1989 (Rel. 12, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Sex pheromone cAM373 (Clumping-inducing agent) (CIA).
Enterococcus faecalis (Streptococcus faecalis).
Bacteria, Firmicutes, Lactobacillales, Enterococcaceae, Enterococcus.
NCBL TaxID=1351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Obta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
"Identification and properties of the prosthetic group of choline oxidase from Alcaligenes sp.";
J. Blochem. 88:197-203 (1980).
J. CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2) PIR; A15398; A15398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
J. Biol. Chem. 263:14574-14578(1988).
-!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMOLVSIN PLASMID PCF10.
PIR; A30812; A30812.
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Alcaligenaceae; Alcaligenes.
NCBI_TaxID=512;
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-!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
-HARBORING PAM373.
-!- HARBORING PAM373.
-!- MISCELLANBOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR SPECIFICITY OF PHEROMONES TO PLASMIDS.
                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                27.3%; Score 9; DB 1; Length 7;
100.0%; Pred. No. 1.46+05;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 27.3%; Score 9; DB 1; Length 7; Similarity 100.0%; Pred. No. 1.4e+05; 2; Conservative 0; Mismatches 0; Indele
                                                                                                                                           7 AA; 790 MW; 72C9D2C731B2C740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AA; 839 MW; 7415B1E457644AC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
Choline oxidase (EC 1.1.3.17) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 AA.
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                                                                                                                                                                                                                              Local Similarity 100.
nes 2; Conservative
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CCF1_ENTFA STANDARD; PRT; 7 AA.
P20104;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Sex pheromone CCF10.
Bactoria felocalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCB1_TAXID=1351;
TISSUE=Fibroblast;
MEDLINE=5009907; PubMed=7523108;
METLINE 35009907; PubMed=7523108;
METLINE 35009907; PubMed=7523108;
METLINE 35009907; PubMed=7523108;
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-I- MISCELLANBOUS; On the 2D-gel the determined pl of this unknown protein is: 6.6, its MM is: 19 kDa.

NON TER
SEQÜENCE 5 AA; 717 MW; 7364087043100000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flengard R., Skjelan L., Plengard R., Skjelan L., Plengard R., Skjelan L., Plengard R., Skjelan L., Proceeding the sequence analysis of proteins from Clostridium pasteurianum WS.", Electrophoresis 19:802-806(1998).

-I MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Unknown protein CP 6 from 2D-page (Fragment).
Clostridium pasteurianum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
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MEDLINE=88008313; PubMed=3139658;
Mori M., Sakagami Y., Ishli Y., Isogai A., Kitada C., Fujino M., Adsit J.C., Dunny G.M., Suzuki A., Structure of CCF10, a peptide sex pheromone which induces conjugative transfer of the Streptococcus faecalis tetracycline resistance plasmid, pCF10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                     27.3%; Score 9; DB 1; Length 5; 66.7%; Pred. No. 1.4e+05; tive 0; Mismatches 1; Indels
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MEDLINE=98291870; PubMed=9629918;
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Best Local Similarity 50.0%,
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Best Local Similarity 66.7<sup>3</sup>
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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ID UNOG_CLOPA
AC P81351;
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-!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP
cyclohydrolase I. This inhibition is reversed by L-phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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01-0CT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
15-MAR-2004 (Rel. 43, Last amnotation update)
UNKNOWN protein from 2D-page of fibroblasts (P19) (Fragment).
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Rodentia; Sciurognathi, Muridae, Musinae; Musinae, Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
GCHFR OR GFRP.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                             rubella.",
Aust. J. Chem. 52:639-645(1999).
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree fro
Litori electrica. Comparison with the skin peptides from Litoria
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0
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-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
Amphibian defense peptide.
SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Liver,
Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
Cowthorne M.,
                                                                                                                                                                                                                                                                                                                                                                                                           Match 33.3%; Score 11; DB 1; Length 5; Local Similarity 100.0%; Pred. No. 1.46+05; les 2; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AA; 806 MW; 71B5B057273B4700 CRC64;
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-!- SUBUNIT: Homodimer (By similarity).
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INIT_MET 0 0
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Best Local Similarity 75.0
Matches 3; Conservative
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P38639;
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mytilus edu
litoria rub
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10-OCT-2003 (Rel. 42, Last sequence update)
Rubellidin 3.1.
Litoria rubella (Desert tree frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae; Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Rubellidin 3.2.
Litoria rubella (Desort tree frog).
Latoria rubella (Desort Netacoa; Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
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P82071
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P41966
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SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                          s AA
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PAP2 PARMA
REIL LITRU
SUGA ACHDO
TPIS CANFA
UC22 MAIZE
ACPH MAIZE
CIP1 MYTED
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RE31_LITRU
ID RE31_LITRU
AC P82072;
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AC P82073;
DT 28-FEB-2003
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DT 10-OCT-2003
DE LICOTA-2003
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DE AMPHIDIA: Ba
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                                                                                                       June 1, 2004, 10:41:50 ; Search time 7.66667 Seconds (without alignments) 47.542 Million cell updates/sec
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             GenCore version 5/1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Listing first 45 summaries
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GFRP_MOUSE
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CCF1_ENTFA
CTA_ENTFA
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Gaps

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T-cell receptor beta chain V-D-J region (141-1BC) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Dacession: P10572; #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: P10574
R;Feeney, A.J.
J; Exp. Med. 114, 115-124, 11991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: P10509; MUID:91277601; PMID:1711558
A;Accession: P70577
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1BC
A;Status: translation not shown
A;Accession: P70574
A;Status: translation not shown
A;Accession: P10574
A;Status: translation ct shown
A;Accession: P10574
A;Status: translation ct shown
A;Accession: P10574
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1Q
C;Keywords: T-cell receptor
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.Title: Unctional sequences of fetal T cell receptor beta chains have few N regions.
.Reference number: PT0509; MUID:91277601; PMID:1711558
.Accession: PT0565
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;Species: Mus musculus (house mouse)
;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
;Accession: PT0565
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A;Molecule type: mRNA
A;Residues: 1-5 <FEE
A;Experimental source: day 19 fetal thymus, strain BALB/C
C;Keywords: T-cell receptor
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Search completed: June 1, 2004, 11:19:23 Job time: 11.6667 secs

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phosphoprotein, bone - chicken (fragment)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus
Cibacession: S11127; S11128
Ribikuni-Takagaki, Y., Gilmcher, M.J.
Biochem. J. 268, 588-591, 1990
A;Title: Post-translational processing of chicken bone phosphoproteins. Identifica: A;Seference number: S11127; MUD:90303246; PMID:2363696
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regic
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0525
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0525
R;Feeney, A.J.
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                               A)Accession: A44955
A)Status: preliminary
A)Molecule type: protein
A)Residues: 1-5 ePQ>
C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase
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           A; Reference number: A44955; MUID:90175700; PMID:2626493
                                                                                                                                                                                                Query Match
27.3%; Score 9; DB 2; Le
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1.
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A;Molecule type: mRNA
A;Residues: 1-5 <FBS>
A;Residues: 1-5 <FBS>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor
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Similarity 33.3%;
1; Conservative ;
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A;Molecule type: protein
A;Residues: 'X',2-5 <MIK2>
C;Keywords: phosphoprotein
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A;Residues: 1-5 <MIK1>
A;Accession: S11128
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Matches 1; Conserv
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                                                                                                                                                                                                                                                                                                                                                                            Glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)

Nathernate names: glycogen phosphorylase b
C;Alterate names: glycogen phosphorylase b
C;Bate: Liza ramada
C;Date: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
C;Accession: A60521
R;Bonamusa, L; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
A;Reference number: A60521; MUID:90227907; PMID:2109669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: A60521.
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-5 <BON>
C;Superfamily: glucan phosphorylase
C;Superfamily: glucan phosphorylase
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experin
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R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
J. Bacteriol. 173, 3564-3572, 1991
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seq
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C;Species: 03-Unn-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
C;Accession: A44952
R;Paquatte, O.; Tu, S.C.
Photochem. Photobiol. 50, 817-825, 1989
A;Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib
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Species: Salmonella typhimurium
Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
                                                                                                                                            Gaps
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A;Cross-references: EMBL:U31309; NID:9974285; PID:9974292
A;Experimental source: strain s6PT2x86PT3; 8 month seedlings
                                                                                Query Match 27.3%; Score 9; DB 2; Length 4; Best Local Similarity 33.3%; Pred. No. 2.8e+05; Matches 1; Conservative 2; Mismatches 0; Indela
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A)Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 < VOG>A;Cross-references: GB:M62408
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1 QIS 3
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Cycochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion Cycochromeria intochondrion Lampetra fluviatilis (river lamprey)
C,Species: mitochondrion Lampetra fluviatilis (river lamprey)
C,Accession: T13892
R,Delarbre, C; Barriel, V; Tillier, S.; Janvier, P.; Gachelin, G.
A,Title: The main features of the craniate mitochondrial DNA between the NDI and IA,Reference number: Z17775; MUID:97398704; PMID:9254918
A,Accession: T13892
A,Accession: T13892
A,Accession: T13892
A,Featus: preliminary; translated from GB/EMBL/DDBJ
A,Featus: preliminary; translated from GB/EMBL/DDBJ
A,Featus: Z1775; MUID:97398704; PMID:9254918
A,Featus: Embl:Y09528; NID:92340016; PIDN:CAA70721.1; PID:94379123
C,Genetics:
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C;Species: Pinus taeda (loblolly pine)
C;Species: Pinus taeda (loblolly pine)
C;Species: Pinus taeda (loblolly pine)
C;Species: Peb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: T46627
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
B;Deaription: Cloning of a chitinase homolog which lacks chitin binding sites and A;Reference number: Z23105
A;Reference number: Z23105
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-4 <CHA>
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()Species Clostridium thermocellum

()Species Clostridium thermocellum

()Species Clostridium thermocellum

()Accession: 140804

R/Mishra, S.; Beguin, P.; Aubert, J.

R/Mishra, S.; Beguin, P.; Aubert, J.

A/Title: Transcription of clostridium thermoncellum endoglucanase genes celf and A/Reference number: 140804; MUID:91100322; PMID:1987137

A/Accession: 140804

A/Accession: 140804

A/Accession: HORD4

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A;Note: COI
C;Keywords: mitochondrion; oxidoreductase
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A;Start codon: TTG
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T14910
C; Species Petroselinum crispum (parsley)
C; Species Petroselinum crispum (parsley)
C; Species Petroselinum crispum (parsley)
C; Accession: T14910
C; Accession: T14910
C; Accession: T14910
A; Ritricher, S; Ledger, S; Hayashi, H; Weisshaar, B; Schafer, E; Frohnmeyer, H.
Mol. Gen. Genet. 257, 555-665, 1998
A; Title: CPRR4a, a novel plant bZIP protein of the CPRF family: comparative analysis of A; Reference number: Z18261; MuID:98265918; PMID:9604882
A; Reference number: T14910
A; Reference proliminary: translated from GB/EMBL/DDBJ
A; Residues: 1-5 <ALR.
A; Residues: 1-5 <ALR.
A; Residues: 1-5 <ALR.
A; Residues: Los <ALR.
A; Residues: EMBL: Y10810; NID:9336904; PIDN:CAA71769.1; PID:93336905
A; Experimental source: ssp. Hamburger Schnitt
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T-Cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)
T-Cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)
C,Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C,Date: 17-Jul-1992
C,Date: 17-Jul
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C;Species: Oryza sativa (rice)
C;Accesion: PS0254
A;Reference number: PS0206
A;Residues: 1-7 <1SU;
A;Residues: Residues: R
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33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Perfect score:
Sequence:
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Minimum DB seq length: 0 Maximum DB seq length: 7

Total number of hits satisfying chosen parameters:

457

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ribosomal protein	æ	hypothetical prote	T-cell receptor be	5507	cytochrome-c oxida	യ	hypothetical prote	glycoden phosphory	flagellar protein	alkanal monooxygen	phosphoprotein, bo		T-cell receptor be				yl oligope	28K ubiquitin-immu	Y protein - human	þ	MHC H2-L antigen -	T-cell receptor be	T-cell receptor be	cytotoxic T-lympho	ŕ	choline oxidase (E	8	- EO
SUMMARIES		1963	A28709	T14910	PT0644	PS0254	T13892	140804	T46627	A60521	E42364	A44955	811127	PT0525	PT0577	PT0565	PT0700	S69237	A60986	A43766	137263	B26206	I65546	PT0518	PT0662	I49424	LO.	A15398	N	2526
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Query Match 39.4%; Score 13; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels

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sex pheromone CAM3 sex pheromone CCF1 omega-gliadine 1'	ribosomal protein glycoprotein compo	DNA topoisomerase T-cell receptor be	gideachilone 3-tian major fat-globule pullulanase (EC 3.	globulin IV alpha hypothetical prote	ribosomal protein ribosomal protein	ribosomal protein R-phycoerythrin al
7 2 A25269 7 2 A30812 7 2 PN0150			7 2 B48394 7 2 PN0649			5 2 139965 5 2 B22565
9 27.3 9 27.3 27.3	9 27.3	2000 2000 2000 2000			8 24.2 8 24.2	8 24.2 24.2
33 33 35 35	333	3 8 8 3 6 9	. B B	4 4 0 1	4 4 4 3	4. 4. 4. 8.

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Tibosonal protein L30 - Streptomyces griseus (fragment)
C;Species: Streptomyces griseus
C;Species: Streptomyces griseus
C;Accession: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 06-Jun-1997
C;Accession: S19630
R;Ochi, K.
Int. J. Syst. Bacteriol. 42, 144-150, 1992
A;Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomyce
A;Feference number: S19630; MUID:92144363; PMID:1736962
A;Accession: S19630
A;Accession: S19630
A;Accession: S19630
A;Accession: S19630
A;Accession: Strain IFO 13189
A;Experimental source: strain IFO 13189
C;Superfamily: Bscherichia coli ribosomal protein L30
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Accession: A28709 E. B. B. R. Mariano, P.S.; Dunaway-Mariano, D. B. B. G. Boloshians, D. B. J. Repburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D. Blochemistry 27, 2229-2234, 1988
A. Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evic
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C;Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)
C;Species: Bacillus cereus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A28709; MUID:88241058; PMID:3132206
A;Accession: A28709
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <0LS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LKISR 7
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Search completed: June 1, 2004, 11:20:18
Job time : 14.6667 secs
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GENERAL IN Application US/08136743B

Sequence 3.1 Application US/08136743B

Sequence 3.1 Application US/08136743B

Sequence 3.1 Application US/08136743B

Sequence 3.1 Application US/08136743B

APPLICANT: Jecroe Salem, and Alison L. Fisher

ITILE OF INVENTION: "Jelasmodium Ribonu-
STREET: 3100 Market Street

CONNETS Enable FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: Instancy Loss

SOFTARE: Belasmodium Ribonu-
ITILE DATE: 1014/33

COMBRITE INVENTION: 455

ATTORNEY APPLICATION DATE: 1014/33

TELEPHONE: (215) 568-833

TELEPHONE: (215) 568-833

TELEPHONE: (215) 568-833

TELEPHONE: (215) 568-833

TELEPHONE: (215) 568-834

TELEPHONE: CHARACTERISTICS:

NUMBER: No. 54590548

INVENTION: POR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

NUMBER: Anno acids

TWENT: Anno acids
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48.6%; Score 17; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 30+05;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

48.6%; Score 17; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
FILING DATE: 10/14/93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 3957
TELECOMMUICATION INFORMATION:
TELEPHONE: (215) 568-539
TELEPAX: (215) 568-539
TELEPAX: NO. 5459063e
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                    LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-136-743B-31
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Gaps
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                                                                                                                                                                     GENERAL INPORTATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: ILU, CHUAN-FEA
APPLICANT: LIU, CHUAN-FEA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: EDONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT PILING DATE: 1999-10-22
FRIOR APPLICATION NUMBER: 66/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PATENTIN VERSION 3.1
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

88.6%; Score 17; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09233857

Patent No. 6495353

GENERAL INPORMATION:
APPLICANT: Planagan, Peter:
CURRENT PAPLICANTON: HUWAN ORTHOLOGUES OF WART:
FILE REFERENCE: 239/231.
CURRENT FILING DATE: 1999-01-20

FARLIER PILING DATE: 1999-01-21

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-09-428-082B-271
                                                                                                                            Sequence 271, Application US/09428082B
Patent No. 6660843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/08136743B Patent No. 5459063
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: HUMAN
US-09-233-857-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TDF 3
                                                                                                      US-09-428-082B-271
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US-09-233-857-7
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Sequence 30, Application US/08136743B

Patent No. 5459063

GENERAL INFORMATION:

APPLICANT: Barry S. Cooperman, Harvey Rubin,

APPLICANT: Jerome Salem, and Alison L. Fisher

ITLE OF INVENTION: "Plasmodium falciparum Ribonu-

TITLE OF INVENTION: "Percof"

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSE: The University of Pennsylvania

STREET: 310 market Street

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U. S.A.

ZIP: 19104-3246

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
                                                             "Plasmodium falciparum Ribonu-
cleotide Reductase, DNA Sequences Therefor and Peptide in
Thereof"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7;
        APFLICANT: Carry Carry APFLICANT: Carry Carry APFLICANT: Carry Car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
3e+05;
Cooperman, Harvey Rubin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.6%; Score 17; DB 100.0%; Pred. No. 3e+:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.(
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TOF 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY:
US-08-136-743B-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-08-136-743B-30
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eibl, Johann
TITLE OF INVENTION: Factor X Analogues With
a Modified Protease Cleavage Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                     Length 5;
                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94111-3834
COMPUTER READALE DISKette
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OMPUTER: PASTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/367,791A
FILING DATE: 12-No. 6573071-1999
PRIOR APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (415) 576-0200
                                                                                                                                                                Score 17; DB 4;
Pred. No. 3e+05;
                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 3e-
Matches 3; Conservative 0; Mismatches
                   STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-09-367-777-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-09-367-791A-76
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 76, Application US/09367791A
Sequence 76, Application US/09367791A
Patent No. 6573071
GENERAL INFORMATION:
APPLICANT: Himmelspach, Michele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schlokat, Uwe
Dorner, Friedrich
Fisch, Andreas
Eibl, Johann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 76: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'ELEX: <Unknown>
            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
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                                                                                                                                                                                                                                                                              NAME/KEY: Peptide
LOCATION: 1..5
OCHER INFORMATION: /note= "Amino acid sequence
OTHER INFORMATION: encoded by nucleotides 1-15 of SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 48.6%; Score 17; DB 2; Length 5; Best Local Similarity 100.0%; Pred.; No. 3e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLION TIRE: LEBACCHE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISED FOR Windows Version 2.0
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/367,777
FILING DATE: 10-No. 6562598-1999
CLASSIPICATION PATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: AT A 336/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00046
FILING DATE: 27-FEB-1997
ATTORNEY/AGENT INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schlokat, Uwe
Schlokat, Uwe
TITLE OF INVENTION: Factor X Deletion Mutants
and Analogues Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 20695D-000900US
TELECOMOUNICATION INFORMATION:
TELECOMOUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acid
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
US-09-367-777-132

Sequence 132, Application US/09367777

Sequence 132, Application US/09367777

SEQUENCE NO. 6562598

SECTION SECTION:

PELICANT: Himmelspach, Michele

PELICANT: Finencer, Michael

PELICANT: Falkner, Falko-Guenter

Bibl, Johann

Dorner, Friedrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 132:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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PERNETAL INPORMATION:

APPLICANT: TANIGUCHI, Nacyuki
APPLICANT: TANIGUCHI, Ne SHORM
APPLICANT: NISHIKANA, Resushi
APPLICANT: NISHIKANA, Resushi
APPLICANT: NISHIKANA, STO7846cmi
TITLE OF INVENTION: NOVEL N-ACETYLGIUCOSAMINYL TRANSFERASE
TITLE OF INVENTION: GENE CODING THEREFOR AND PROCESS FOR PRODUCTION THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STREET: George Mason Bldg., Washington & Prince Sts.
COUNTRY: United States
COUNTRY: United States
SOFTWARE: Fatentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,230
FILING DATE: 16-MAR-1995
CLASCYPICATION. 41s.
                                                                                                                                             GENERAL INPORMATION:
APPLICANT: Boulanger, Pierre
APPLICANT: Boulanger, Pierre
APPLICANT: Boulanger, Pierre
APPLICANT: Boulanger, Ducie
APPLICANT: Hong, Saw See
APPLICANT: Hong, Saw See
APPLICANT: Hong, Saw See
APPLICANT: Hong, Saw See
APPLICANT: Hong, Say See
TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
CURRENT APPLICATION NUMBER: Us/99/15, 613A
CURRENT APPLICATION NUMBER: FR 97/01005
PRIOR FILING DATE: 1999-01-30
PRIOR FILING DATE: 1997-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,736
PILING DATE: 23-AUG-1993
APPLICATION NUMBER: UP 4-245950
FILING DATE: 24-AUG-1992
                                                                    Sequence 59, Application US/09155613A Patent No. 6420120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08405230 Patent No. 5707846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Phagotope
US-09-155-613A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::|||
2 NYTLT 6
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RESULT 6
US-09-155-613A-59
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Gaps
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encoded by nucleotides 1-15 of SEQ ID NO. 7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.6%; Score 17; DB 1; Length 5; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
                                                                                                                     001560-215
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-237118
                              FILING DATE: 06-AUG-1993
ATTORNEY/AGENT: 1NFORMATION:
NAME: CRANG-PEULY, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 00156
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 3; Conservative
                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: Peptide
; LCCATION: 1..5
; OTHER INFORMATION: /
; OTHER INFORMATION: e
US-08-405-230-10
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US-08-910-990-10 RESULT 8

Sequence 10, Application US/08910990
| Patent No. 5834284
| GENERAL INPORMATION: Navoyuki |
| APPLICANT: TANIGUCHI, Navoyuki |
| APPLICANT: TANIGUCHI, Navoyuki |
| APPLICANT: TANIGUCHI, No. 58342840mi |
| APPLICANT: TANIGUCHI, No. 58342840mi |
| APPLICANT: YAMAGUCHI, No. 58342840mi |
| APPLICANT: YAMAGUCHI, No. 58342840mi |
| TITLE OF INVENTION: GENE CODING THEREFOR AND PROCESS FOR PRODUCTION THEREOF |
| TITLE OF INVENTION: Gene CODING THEREFOR AND PROCESS FOR PRODUCTION THEREOF |
| TITLE OF INVENTION: Base |
| TITLE OF INVENTION: Gene CODING THEREFOR AND PROCESS FOR PRODUCTION THEREOF |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mason Bldg., Washington & Prince Sts. |
| TITLE OF INVENTION: Mas

CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,990
FILING DATE:

CLASSIFICATION 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/405,230
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: US 08/110,736
FILING DATE: 23-AUG-1993
APPLICATION NUMBER: UP 4-245950
FILING DATE: 24-AUG-1992
PRIOR APPLICATION NUMBER: UP 5-237118
FILING DATE: 06-AUG-1993
ATPLICATION NUMBER: UP 5-237118
FILING DATE: 06-AUG-1993
ATPLICATION NUMBER: UP 5-237118
FILING DATE: 06-AUG-1993
ATPLICATION NUMBER: UP 5-237118 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

NAME: Crane-Feury, Sharon E REGISTRATION NUMBER: 36,113

```
GENERAL INFORMATION:

APPLICANT: Lo, Reggie Y.C.

APPLICANT: Botter, Anthony B.

APPLICANT: Schryvers, Anthony B.

APPLICANT: Potter, Andrew A.

TITLE OF INVENTION: FASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME

TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME

TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME

TILE OF THE SPETIMENT APPLICATION NUMBER: US/08/753,750B

CURRENT APPLICATION NUMBER: C2,164,274

PRIOR FILING DATE: 1995-12-01

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FASTENCY PASTEUR BOSTE: 1995-12-01

NUMBER: SAG ID NOS: 68

SOFTWARE: FASTENCY PASTEUR BOSTE: CA Windows Version 4.0

SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó.
                     APPLICANT: HELLYER, Susan A.
APPLICANT: DE SILVA, Jacqueline
APPLICANT: WHITEMAN, Sally A.
ITILE OF INVENTION: Tomato Xyloglucan Endo-Transglycosylase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.3%; Score 19; DB 4; Length 7; 60.0%; Pred. No. 3e+05; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 3;
Pred. No. 3e+05;
0; Mismatches
                                                                                                                                                                                                            STATE: D.C.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPRATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,737
FILING DATE: 06-MAY-1996
CLASSIFICATION: 800
PRICK APPLICATION BATA:
APPLICATION NUMBER: PCT/GB94/02467
FILING DATE: 10-NOV-1994
PRICK APPLICATION NUMBER: GB 932325.4
FILING DATE: 10-NOV-1993
INPORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/08753750B
Patent No. 6610506
    ARROWSMITH, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Bscherichia coli
US-08-753-750B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DFTLT 6
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                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Yong Sig KIM
APPLICANT: Son Chung PARK
APPLICANT: Hosull LEE
APPLICANT: Gong Woo CHO
APPLICANT: Chang H. CHONG
APPLICANT: Chang H. CHONG
TITLE OF INVENTION: Amaranthus Viridis, DNAs Encoding Therefrom
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                      Ouery Match 54.3%; Score 19; DB 4; Length 6; Best Local Similarity 80.0%; Pred. No. 38+05; Matches 4; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ Floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WOORDER-EGE 6.1 Windows
CURRENT APPLICATION DATA:
FILING DATE: 22 AUG 1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08916443A Patent No. 6001986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 38, Application US/08640737; Patent No. 6215044; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTONNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 1945
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
; LOCATION: ()...(); OTHER INFORMATION: Epitope tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 50.0
Matches 3, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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US-08-640-737-38
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Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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ORGANISM: unknown
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDFTL 5
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Unknown
FEATURE:
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999999999999999
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LENGTH: 6
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                                                                     June 1, 2004, 11:13:51; Search time 13.6667 Seconds (without alignments) 26.443 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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Sequence
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

// cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

// cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

// cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

// cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

// cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

// cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
      GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-916-443A-8

US-08-640-737-38

US-08-155-613A-59

US-08-155-613A-59

US-08-10-990-10

US-08-10-990-10

US-09-367-777-132

US-09-367-777-132

US-09-367-777-132

US-09-367-777-132

US-08-136-743B-29

US-08-136-743B-31

US-08-136-743B-31

US-08-136-743B-32

US-08-136-743B-32
                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                   389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                   US-09-712-819C-5
35
1 TDFTLTI 7
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Match Length
                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 7
                                                                                                                     Title:
Perfect score:
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No.
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Sequence 17, Appl
Sequence 23, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 18, Appl
Sequence 7, Appli
Sequence 18, Appl
Sequence 55, Appl
Sequence 55, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
                                                                                                                     Sequence 5, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 28, Appl
Sequence 52, Appl
Sequence 52, Appl
Sequence 1746, Appl
US-09-166-205B-14

US-09-611-411-17

US-09-611-411-13

US-09-611-451-26

PCT-US94-02629-14

US-08-252-29550-7

US-08-482-528-180

US-08-482-528-180

US-08-482-528-180

US-08-482-528-180

US-08-17-108A-7

US-08-17-109A-7

US-08-17-109A-7

US-08-17-109A-7

US-08-17-109A-7

US-08-17-109A-7

US-08-17-109A-7

US-08-17-109A-7

US-08-17-10-1

US-09-040-216-28

US-09-040-216-28

US-09-040-216-28

US-09-040-216-28

US-09-040-216-28

US-09-040-216-28
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## ALIGNMENTS

```
RESULT 2
US-09-774

US-09-774-297-4

Sequence 4, Application US/09724297

Sequence 4, Application US/09724297

Patent No. 642338

GENERAL INFORMATION:

APPLICANT: The Board of Trustees of the University of Illinois

APPLICANT: Wittrup, et al.

TITLE OF INVENTION:

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/724,297

CURRENT APPLICATION NUMBER: US 09/009,388

PRIOR APPLICATION NUMBER: US 09/009,388

PRIOR PILING DATE: 1998-01-20

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.0
US-09-140-084-4

Sequence 4, Application US/09140084A

Sequence 4, Application US/09140084A

Patent No. 6300065

GENERAL INFORMATION:

APPLICANT: Kieke, et al.

TITLE OF INFORMATION:

FILE REFERENCE: D6061C1P2

CURRENT APPLICATION NUMBER: US/09/140,084A

CURRENT FILING DATE: 1998-08-26

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 4
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0
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US-09-140-084-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 4; Length 6;
Pred. No. 3e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.3%;
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Sequence 107, Application US/09788006
Publication No. US20030036093A1
GENERAL INFORMATION:
Publication No. US20030036093A1
GENERAL INFORMATION:
APPLICANT: Klepeis, John L.
TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and TITLE OF INVENTION: Polypeptide Tertiary Structures
FILE REFERENCE: PU-0007
FILE REFERENCE: PU-0007
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patehtin version 3.0
SEQ ID NO 107
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 108, Application US/09788006
Publication No. US20030036093A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL Floudes, Christopher A.
APPLICANT: Floudes, Christopher A.
APPLICANT: Floudes, Christopher A.
APPLICANT: Klepeis, John L.
TITLE OF INVENTION: Polypeptide Tertiary Structures
FILE REPERENCE: PU-0007
TITLE OF INVENTION: PO19788,006
CURRENT FALING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
SEQ ID NO 108
LENGTH: 5
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Query Match 51.4%; Score 18; DB 14; Length 7; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 4; Conservative 0; Mismatches 0; Indels
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Pred. No. 1e+06;
1; Mismatches 0; Indels
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Pred. No. 1e+06;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT; ORGANISM: Streptomyces griseus
US-09-788-006-108
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Best Local Similarity 75.0%;
Matches 3; Conservative
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Best Local Similarity 75.0%;
Matches 3; Conservative
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US-09-788-006-108
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Sequence 11, Application US/10349507

Publication No. U320031099002A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hekimi, Siegfried
APPLICANT: Benard, Claire
APPLICANT: Benard, Claire
APPLICANT: Benard, Claire
APPLICANT: McCright, Brenton
APPLICANT: McCright, Brenton
APPLICANT: NCLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
FILE REFERENCE: 11202-006-999
CURRENT APPLICATION NUMBER: US/10/349,507
CURRENT FILING DATE: 2003-01-22
PRIOR PLING DATE: 2003-01-22
PRIOR PPLICATION NUMBER: PCT/CA01/00913
PRIOR PLING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/213,174
PRIOR PPLING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/213,174
PRIOR PPLING DATE: 2000-06-22
PRIOR PLING DATE: 2000-06-22
PRIOR PLING DATE: 2000-06-22
PRIOR PLING DATE: 2000-06-22
                                                                                                             APPLICANT: POGLASKI, FEARLY
APPLICANT: POGLASKI, FEARLY
APPLICANT: STEER, Alvin
APPLICANT: STEER, Alvin
TITLE OF INVENTION: LYPEPICATION AND CHARACTERIZATION OF CYTOTOXIC
TITLE OF INVENTION: LYPEPICATION FACTOR AND MONOCLONAL
TITLE OF INVENTION: ANTIBODIES THERETO
TITLE OF INVENTION: ANTIBODIES THERETO
TITLE OF INVENTION: ANTIBODIES THERETO
CURRENT APPLICATION NUMBER: US/10/267,565
CURRENT APPLICATION NUMBER: 08/459,151
PRIOR APPLICATION NUMBER: 08/459,151
PRIOR APPLICATION NUMBER: 08/459,151
PRIOR PILING DATE: 1992-06-22
PRIOR PILING DATE: 1992-03-24
PRIOR PILING DATE: 1992-03-24
PRIOR PILING DATE: 1990-06-27
PRIOR PILING DATE: 1990-06-27
PRIOR PILING DATE: 1990-06-27
PRIOR PILING DATE: 1990-06-09
PRIOR PILING DATE: 1990-05-09
PRIOR PILING DATE: 1990-12-22
NUMBER OF SEQ ID NOS: 43
SOFTWARE: RESERVED FOR WINDOWS Version 3.0
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Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRGANISM: Homo sapiens
US-10-267-565-11
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US-10-156-820-59
Sequence 59, Application US/10156820
Sequence 59, Application US/10156820
Sequence 59, Application US/10156820
Sequence 59, Application US/10156820
Sequence 59, Application No. US20020150558A1
GENERAL INFORMATION:
THE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
STILE REFERENCE: 032751-036
CURRENT APPLICATION NUMBER: US/10/156,820
CURRENT APPLICATION NUMBER: US/206-30
PRIOR FILING DATE: 1998-01-30
PRIOR PELING DATE: 1997-01-30
PRIOR PELING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 98
SOPTWARE: PastSEQ for Windows Version 4.0
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APPLICANT: Mazur, Wieslaw A
ITILE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8847M
CURRENT APPLICATION NUMBER: US/10/317,252A
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/349,117
PRIOR PLING DATE: 2002-01-16
PRIOR PLING DATE: 2002-04-29
PRIOR PLING DATE: 2002-04-29
PRIOR PLING DATE: 2002-04-29
PRIOR PLING DATE: 2002-06-14
PRIOR PLING DATE: 2002-06-14
PRIOR PLING DATE: 2002-06-14
PRIOR PLING DATE: 2002-06-15
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 530
SOFTWARE: Patentin version 3.2
SEQ ID NO 402
LENGTH. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB 14; Length 6; Pred. No. 1e+06; 0; Mismatches 1; Indels
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US-10-267-565-11
Sequence 11, Application US/10267565
Publication No. US20030204059A1
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80.0%;
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ORGANISM: Artificial Sequence
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CTHER INFORMATION: Phagotope
US-10-156-820-59
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: artificial
FEATURE:
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Gaps

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0; Indels

TYPE: PRT CORGANISM: Homo sapiens US-10-349-507-11

Gaps

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Publication No. US20030148957A1

Publication No. US20030148957A1

Publication No. US20030148957A1

GENERAL INFORMATION:

APPLICANT: The Procter & Gamble Company

APPLICANT: Isfort, Robert J

APPLICANT: Maculaw A

TITLE OF INVENTION: Cottcotropin Releasing Factor 2 Receptor Agonists

TITLE REPERSENCE: 8407M2

CURRENT APPLICATION NUMBER: US/10/317,251A

FRIOR FILING DATE: 2002-01-16

PRIOR FILING DATE: 2002-01-16

PRIOR PLILING DATE: 2002-04-29

PRIOR PLILING DATE: 2002-04-29

PRIOR PLILING DATE: 2002-04-29

PRIOR PLILING DATE: 2002-06-14

PRIOR PLILING DATE: 2002-06-14
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US-10-315-964A-402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Chemically synthesized artificial peptide US-10-317-251A-402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 54.3%; Score 19; DB 14; Length 6; Best Local Similarity 80.0%; Pred. No. 1e+06; Matches 4; Conservative 0; Mismatches 1; Indels
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    PRIOR APPLICATION NUMBER: US 60/349,117
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: US 60/376,337
PRIOR FILING DATE: 2002-04-29
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 530
SOFTWARE: PALENTIN VENSION 3.2
SEQ ID NO 402
LENGTH: 6
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Best Local Similarity 80.0
Matches 4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: artificial
FEATURE:
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2 TKFTL 6
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US-10-317-252A-402
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                                                                                                                 APPLICANT: Clevener, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING
TITLE OF INVENTION: EMDOGENOUS IMHIBITOR OF ATP SYNTHASE, INCLUDING
TITLE OF INVENTION: TREATMENT FOR DIABETES
FILE REFERENCE: 660088 43551
CURRENT APPLICATION NUMBER: US/09/796,076
CURRENT FILING DATE: 2001-02-27
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PREUSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 6
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APPLICANT: The Proces & Gamble Company
APPLICANT: Isfort, Robert J
APPLICANT: Mazur, Wieslaw A
TITLE OF INVENTION COrtcotropin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8647M3
CURRENT APPLICATION NUMBER: US/10/315,964A
CURRENT PILING DATE: 2003-04-01
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Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.3%; Score 19; DB 14; Length 6; 80.0%; Pred. No. 1e+06; vative 0; Mismatches 1; Indels
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Publication No. US20030148956A1
GENERAL INFORMATION:
Publication No. US20040072739A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Epitope tag
US-09-796-076-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Epitope tag
US-10-083-815-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.0
Matches 4; Conservative
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US-10-315-964A-402
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Gaps

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Sequence 122, Application US/10351891
| Publication No. US20040048311A1 |
| GENERAL INFORMATION: |
| APPLICANT: DANA AUT.-RICHE |
| TITLE OF INVENTION: USE OF COLLECTIONS OF BINDING SITES FOR SAMPLE PROFILING AN |
| TITLE OF INVENTION: APPLICATION APPLICATIONS OF BINDING SITES FOR SAMPLE PROFILING AN |
| FILE REPERENCE: 25885-1753 |
| CURRENT APPLICATION NUMBER: US/10/351,891 |
| CURRENT APPLICATION NUMBER: US 60/352,011 |
| PRIOR FILING DATE: 2002-01-24 |
| NUMBER OF SEQ ID NOS: 140 |
| SEQ ID NO 122 |
| LENGTH: 6 |
| CONTACT OF THE CONTACT ON THE CONTACT OF THE CONTACT ON THE CONTACT OF THE CONTACT OF THE CONTACT ON THE CONTACT
   Sequence 394, Application US/10317252A
Publication No. US20030148958A1
GENERAL INFORMATION:
APPLICANT: The Proceer & Gamble Company
APPLICANT: Tiefort, Robert J
APPLICANT: Macur, Wieslaw A
TITLE OF INVENTION: Correctopin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8847M
CURRENT FILING DATE: 2002-03-31
PRIOR PLICATION NUMBER: US 60/349,117
PRIOR PLICATION NUMBER: US 60/349,117
PRIOR PLILING DATE: 2002-01-16
PRIOR PLILING DATE: 2002-04-29
PRIOR PLILING DATE: 2002-04-29
PRIOR PLILING DATE: 2002-06-14
PRIOR PLILING DATE: 2002-06-14
PRIOR PLILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 530
SOFTAMER PARENTALING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 530
SOFTAMER PARENT PARENTIN VERSION 3.2
LENGTH: 5
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0
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US-10-317-252A-394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.3%; Score 19; DB 14; Length 5; 80.0%; Pred. No. 1e+06; 1ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 12; Length 6; Pred. No. 1e+06; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.3%;
80.0%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -10-351-891-122
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HPPLICANT: Mazur, Wieslaw A

TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
FILE REPERENCE: 8847M3
CURRENT APPLICATION NUMBER: US/10/315,964A
CURRENT FILING DATE: 2003-04-01
PRIOR PLING DATE: 2002-01-16
PRIOR PLING DATE: 2002-01-16
PRIOR PLING DATE: 2002-04-29
PRIOR PLING DATE: 2002-04-29
PRIOR PLING DATE: 2002-06-14
PRIOR PLING DATE: 2002-06-14
PRIOR PLING DATE: 2002-06-19
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 530
SOFTWARE: Patentin Version 3.2
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: The Procter & Gamble Company
APPLICANT: The Procter & Gamble Company
APPLICANT: The Procter J
APPLICANT: Mazur, Wieslaw A
TITLE OF INVENTION: Cortcortopin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8847M2
CURRENT FILING DATE: 2002-11
PRIOR FILING DATE: 2002-01-16
PRIOR PLICATION NUMBER: US 60/349,117
PRIOR PLICATION NUMBER: US 60/376,337
PRIOR PLILING DATE: 2002-06-14
PRIOR PLILING DATE: 2002-06-14
PRIOR PLILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 530
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h Similarity 80.0%; Pred. No. 1e+06; 4; Conservative 0; Mismatches 1; Indele
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; Sequence 394, Application US/10317251A
; Publication No. US20030148957A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: artificial
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ORGANISM: artificial
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Matches
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; Sequence 4, Application US/09796076

RESULT 6 US-09-796-076-4

1 TKFTL 5

RESULT 4 US-10-317-252A-394

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Sequence 271, App
Sequence 271, App
Sequence 271, App
Sequence 131, App
Sequence 271, App
Sequence 271, App
Sequence 271, App
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 37, App
Sequence 37, Appl
Sequence 37, Appli
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TITLE OF INVENTION: Transcriptional Activation System, Activators, and Uses
TITLE OF INVENTION: Therefor
FILE REPERENCE: 0342941-0065
CURRENT APPLICATION NUMBER: US/09/943,944E
CURRENT APPLICATION DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 126
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US-09-943-944E-126
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2 US-10-436-549-151

2 US-10-632-388-271

2 US-10-632-388-271

2 US-10-645-761-271

2 US-10-645-761-271

4 US-10-645-761-271

5 US-10-645-761-271

5 US-10-645-761-271

6 US-10-65-696-271

6 US-10-653-048-271

6 US-10-653-048-271

7 US-10-102A-55

1 US-10-10-19-25

1 US-10-264-309-288

2 US-10-264-309-288

2 US-10-264-309-288

3 US-10-264-309-288

4 US-10-214-796-21

4 US-10-286-186-3

0 US-09-788-006-3

4 US-10-286-186-4

6 US-10-286-186-4

6 US-10-286-186-4

6 US-10-286-186-8

7 US-10-286-186-8

8 US-10-286-186-8

8 US-10-290-886-8

1 US-10-291-886-8

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1 US-10-291-886-8

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2 US-10-291-886-8

4 US-10-291-886-8

4 US-10-291-886-8

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4 US-10-291-886-8

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Sequence 394, Application US/10315964A

Publication No. US20030148956A1

GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Isfort, Robert J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 126, Application US/09943944E; Publication No. US20040014036A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDFTL 5
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US-09-943-944E-126
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Sequence 394, App
Sequence 394, App
Sequence 122, App
Sequence 4, Appli
Sequence 402, Appli
Sequence 402, App
Sequence 402, App
Sequence 59, App
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
                                                                                                                                                                    June 1, 2004, 11:18:42; Search time 34.6667 Seconds (without alignments) 56.387 Million cell updates/sec
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| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/DS06_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-315-964A-394
US-10-317-251A-394
US-10-317-251A-394
US-10-317-251A-394
US-10-351-891-122
US-09-796-076-4
US-10-315-964A-402
US-10-315-964A-402
US-10-315-964A-402
US-10-315-964A-402
US-10-315-964A-402
US-10-315-965-11
US-10-267-565-11
US-10-267-565-11
US-09-788-006-107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1151071 segs, 279249464 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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35
1 TDFTLTI 7
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Match Length
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Perfect score:
Sequence:
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No.
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XX SQ Sequence 6 AA;

Query Match 54.3%; Score 19; DB 3; Length 6; Best Local Similarity 80.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 1; Indels

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q 6

Search completed: June 1, 2004, 11:16:16 Job time: 47.6667 secs

The present invention relates to a method for selecting proteins for displayability on a yeast cell surface. The method comprises transforming yeast cells with a vector that expresses a test protein fused to a yeast cell will mail protein fused to a yeast cells with a label that binds to proteins displayed on the cell wall, and isolating label bound cells, where the test protein is from a variegated population generated by mutagenesis. The invention is also directed to new processes for engineering T cell receptor for improved binding properties. Improved T cell receptor molecules are useful in therapies for cancer, sepsis, autoimmus diseases such as arthritis, diabetes or multiple sclerosis. The methods are useful to select proteins with altered affinity, altered specificity or conditional binding. The present sequence is an epitope tag fused between protein of interest and yeast cell wall protein AGA2

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Selecting proteins with enhanced phenotypic properties than wild-type proteins, is useful for highly specific cancer diagnosis and therapy.
                                                                                                                                                                                                                                                                                                                                                                                  Yeast cell wall protein, AGA2; T cell receptor, multiple cancer; sepsis; autoimmune disease; arthritis; diabetes.
                                                                                                                                                                                                                                                                                                                                                                   Epitope tag #2 fused to yeast cell wall protein AGA2.
                                                                                                                                                                                                                                                                                                                    AAE16558 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 40; Col 60; 59pp; English.
       98US-00009388.
98US-00140084.
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97US-00866398.
                              (UNII ) UNIV ILLINOIS FOUND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNII ) UNIV ILLINOIS FOUND.
                                                                                                                                                                                                                                                                                                                                                   09-APR-2002 (first entry)
                                              Wittrup KD, Kieke MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kranz DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-430619/36.
                                                                                                                                                                                                                                                               1 TDFTL 5
                                                                                                                                                                                                                 Sequence 6 AA;
       20-JAN-1998;
26-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                         US6331391-B1.
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                                                                                                                                                                                                                                                                                                                                                                                 feast cell
                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                         Selecting proteins with enhanced phenotypic properties than wild-type proteins, is useful for highly specific cancer diagnosis and therapy.
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Pred. No. 1.4e+06;
0; Mismatches 1; Indels
   Boder ET
Shusta E,
                                                                                                                                                                                                                                Disclosure; Page 7; 116pp; English.
Kranz DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.3%;
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Best Local Similarity 80.0
Matches 4; Conservative
                                                            WPI; 1999-430619/36.
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Length 6;

Sequence 6 AA;

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The invention relates to a method for identifying compounds which inhibit internalization of cells surface receptors. Provided are an array of locations, each containing cells with a cell surface receptor protein, that are treated with a test compound. The protein is luminescently labeled or contacted with a luminescence produced is converted into test compound treatment. Any luminescence produced is converted into digital data and automatically analysed to determine if the test compound induced the protein internalization. The novel method is used to screen internalization, this can be used in drug discovery, to test compound internalization, this can be used in drug discovery, to test compound compact. It has high throughput and uses smaller volumes of reagents and test compounds. Sequences AAY7704-718 represent examples of peptide epitope tags used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Automated screening method for identifying compounds which induce cell surface receptor internalization, useful for drug discovery.
                                   Gaps
                                   .;
0
                                                                                                                                                                                                                                                                                                  Cell surface receptor; luminescence; protein internalization; drug discovery; screening assay; epitope; AU5.
                                 1; Indels
Score 19; DB 2; I
Pred. No. 1.4e+06;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunlay T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Page 67; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gough A,
                                                                                                                                                                        AAY77708 standard; peptide; 6 AA.
 54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US015870,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0092671P
                                                                                                                                                                                                                                      12-MAY-2000 (first entry
                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rubin RA, Giuliano KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CEPT-) CEPTOWICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-171170/15.
                                                                                                                                                                                                                                                                    AUS peptide epitope
Query Match
Best Local Similarity
                                                             1 TDFTL 5
                                                                                           TDFYL 5
                                                                                                                                                                                                                                                                                                                                                                                WO200003246-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                              20-JAN-2000
                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                      AAY77708;
                                 datches
                                                                                                                                            RESULT 15
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sclerosis;

Boder

Kieke M,

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The invention relates to a novel non-native peptide derived from corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides have the following activities: myopachic, osteopathic, hypotensive, cardiant, vasotropic, antidiabetic, analgesic, antiallergic, notropic, antidiabetic, analgesic, antiallergic, corticopic, antidiabetic, analgesic, antiallergic, nationallizer, anxiolytic, antidiabetic, analgesic, antiallergic, control of pervent or related compounds derived from other proteins, care used to prevent or treat disorders modulated by the CRF2 receptor, caused, heart/circulatory diseases (e.g. hypertension, congestive heart fallure, heart attack, reperfusion injury, migraine, stroke, memory loss, allure, heart attrack, reperfusion injury, migraine, stroke, memory loss, allure, heart attricis); metabolic disease (obseity or diabetees); pain, allergy; stress; anxiety; low levels of adrenocorticotrophic hormone; anorexia nervosa; depression; also to reduce body temperature and to control appetite or organitive function. Nucleic acids optionally labelled, that encode the non-native CRF2 peptides are used as primers and probes for amplification, also for gene synthesis and for recombinant therapy. Antibodies specific for the non-native CRF2 peptides are used to evaluate expression of the non-native CRF2 peptides are used to evaluate expression of the non-native CRF2 peptides after gene therapy.

This sequence represents a CRF2 non-native polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                    New non-native peptide derived from corticotropin-releasing factor-2, useful for treatment and prevention of e.g. muscular atrophy, also related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Epitope tag, antibody engineering, yeast, surface display,
protein library, peptide library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.3%; Score 19; DB 7; Length 5; 80.0%; Pred. No. 1.4e+06; 1ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 394; 300pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY06466 standard; peptide; 6 AA
                                                   16-JAN-2002; 2002US-0349117P.
29-APR-2002; 2002US-0376337P.
14-JUN-2002; 2002US-0388895P.
19-SEP-2002; 2002US-0411988P.
16-JAN-2003; 2003WO-US001451
                                                                                                                                                                                                  (PROC ) PROCTER & GAMBLE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                WPI; 2003-787974/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TDFTL 5
| | | |
1 TKFTL 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Epitope tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY06466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
AAY06466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel non-native peptide derived from corticotropin-releasing factor-2 (GRF2). The CRF2 peptides have the following activities impopabilic, osteopathic, hypotensive, cardiant, vasotropic, antidiabetic, analgesic, antiallergic, tranquilizer, antidiabetic, antidiathritic. The CRF2 peptides, and antidiathritic. The CRF2 peptides, and cardiant, and antidathritic. The CRF2 peptides, and created compounds derived from other proteins, as used to prevent or treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle atrophy or wasting, and bone disorders, however caused, heart discalatory reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease, reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease, ceperfusion injury, migraine, stroke, memory loss, Alzheimer's disease, ceperfusion injury, migraine, stroke, memory loss, Alzheimer's disease, ceperfusion injury, migraine, stroke, memory loss, Alzheimer's disease, obesity or diabetes); pain allorgy; stress; anxiety; low levels of adrenocorticotrophic hormone, anorexia nervosa; depression, also to reduce body temperature and to control appetite or cognitive peptides are used as primers and probes for amplification, also for gene synthesis and for recombinant production of GRF2 peptides, including use in gene therapy. Antibodies specific for the CRF2 peptides, including use valuate expression of the CRF2 peptides after gene therapy. This sequence represents a novel native CRF polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-native; corticotropin-releasing factor-2; CRF2; myopathic; osteopathic; hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective; nootropic; neuroprotective; antidiabetic; analgesic; antidiapetic; analgesic; antidepressant;
                                                                                                                                                                                                                                                                                                                                     New non-native peptide derived from corticotropin-releasing factor-2, useful for treatment and prevention of e.g. muscular atrophy, also related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 54.3%; Score 19; DB 7; Length 5; Best Local Similarity 80.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRF2 non-native polypeptide, SEQ ID No 394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 394; 304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE51377 standard; peptide; 5 AA.
                     16-JAN-2002; 2002US-0349117P.
29-ARP-2002; 2002US-037837P;
44-JUN-2002; 2002US-0388895P.
19-SEP-2002; 2002US-0411988P.
                                                                                                                                                                 (PROC ) PROCTER & GAMBLE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2004 (first entry)
                                                                                                                                                                                                                        Isfort RJ, Mazur WA;
                                                                                                                                                                                                                                                                                 (PI; 2003-787975/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE51377;
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Gaps . 0

1; Indels

99WO-US001188.

20-JAN-1999;

22-JUL-1999.

W09936569-A1.

WO2003062268-A2

31-JUL-2003

Unidentified

RESULT 12
ADE51377
ID ADE51377
XX
AC ADE51
XX
DT 29-JAN
XX
XX
CCF2 1
XX
XX
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XX
XX

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Example of peptide 2 for treatment of schizophrenia or psoriasis.

AAP82200 standard; protein; 5 AA.

25-OCT-1990

AAP82200;

schizophrenia; psoriasis; vasoactive intestinal polypeptide.

87SE-00000125. 87SE-00000125

15-JAN-1987; 15-JAN-1987;

SE8700125-A. 16-JUL-1988.

Synthetic.

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Activating sequence, Gal4; transcriptional activator, RNA polymerase, Protein-protein interaction, gene therapy; therapeutic, holoenzyme;
                                        Transcriptional activator peptide fragment LS130.
     AAW31467 standard; protein; 6 AA.
                                                                                                               97WO-US007338
                                                                                                                           96US-0017016P
97US-00017016
                            04-AUG-1998 (first entry)
                                                                Gall1; DNA binding domain
                                                                                                                                                         Lu X, Wu Y;
                                                                                                                                           (HARD ) HARVARD COLLEGE
                                                                                                                                                                    WPI; 1998-018502/02.
N-PSDB; AAV02565.
                                                                                                               02-MAY-1997;
                                                                                                                           03-MAY-1996;
01-MAY-1997;
                                                                                       W09744447-A2
                                                                                                   27-NOV-1997
                                                                                                                                                        Ptashne M,
                                                                            Synthetic.
                 AAW31467;
AAW31467
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fragments used in an assay to determine novel transcriptional activators.

It fragments used in an assay to determine novel transcriptional activators.

The method involves the production of transcriptional activators.

Comprising of a DNA-binding group and does not represent a comprising of a natural transcription activator. Protein-protein

Covalently bonded to the DNA binding group and does not represent a comprising of a natural transcription activator. Protein-protein

Covalently bonded to the DNA binding group and does not represent a contractions are identified in the assay by fusing a DNA-binding domain can alibrary of DNA fragments and introducing this and a fusion of target to a library that interact with the target from activation of transcription.

Covalently den a polypoptide containing a region of Gal4 which interacts with the target from activation of transcription.

Covalently den activity, particularly in gene therapy (e.g. recognizing a site close to a selected therapeutic gene). Transcription can be activated without blocking other transcriptional activators. They probably act by interacting with a component of the RNA polymerase II

Choloenzyme, Galli, the strongest known yeast activator, which provides a interactions. Such activators do not create toxicity problems even when
New transcriptional activator containing DNA binding domain bound to peptide - useful for controlling gene expression, especially in gene therapy, and in protein-protein interaction assays, does not inhibit other transcription activators.
                                                                                                                                                                                                                                                                                                                 Example 1; Page 26; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6 AA;
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corticotropin-releasing factor-2; CRP2; myopathic; osteopathic; hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective; nootropic; neuroprotective; anorectic; antidiabetic; analgesic; antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                        Corticotropin-releasing factor-2 polypeptide, SEQ ID No 394.
                                                                                                                                                                                                                                                                                                         54.3%; Score 19; DB 1; Length 5; 75.0%; Pred. No. 1.4e+06; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           ADE65091 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2003; 2003WO-US001454.
                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                          3; Conservative
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         1 TDFT 4
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                                                                                                                                                                                                                                                                                            Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                           ADE65091;
Matches
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Specific example of pentapeptide of the general formula of AAP82197.
These peptides can be administered intravenously, topically or perorally to relieve the symptoms of psoriasis or schizophrenia. Amino acids at posms 2 and 3 can be any residue but Asp is preferred at posm 3. See also

AAP82196-9

Short peptide(s) for treatment of psoriasis and schizophrenia - comprise

WPI; 1988-328337/46.

Wetterberg L;

(WETT/) WETTERBERG

Claim 1; Page 5; 9pp; Swedish.

aminoacid(s)

TOFLL

Gарв .; 0

1; Indels

Query Match 57.1%; Score 20; DB 2; Length 6; Best Local Similarity 80.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 1; Indels

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Gaps

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(NIHA ) JAPAN ENERGY CORP.
                          (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-350322/30.
                                                                                                                                     4PI; 2000-665002/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DFTLTI 7
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DFTLSI 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-0CT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-1997;
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110 AAY1

AAY1

AAY1

XX AAY1

XX AAY1

XX AAY1

XX COUP

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The invention relates to diagnosing the presence of colon cancer, metastases of colon cancer, staging colon cancer, monitoring colon cancer for the onset of metastasis or monitoring a change in stage of colon cancer in a patient. The method involves determining a colon specific gene (CSG) in cells, tissues or bodily fluids and comparing it with levels of CSG in cells, tissues or bodily fluids from a normal human control. Colon cancer can be treated by administering a molecule which down regulates the expression or activity of CSG. An immune response is mounted. Therefore to a cSG protein to a patient, so that a nimmunologically stimulatory amount of a CSG protein to a patient, so that an immunologically stimulatory amount of a CSG protein to a patient, so that colon cancer in a patient by administering an agent labelled with paramagnetic ions or a radioisotope to the patient. They are also useful for preventing the onset of colon cancer, and in diagnosis and treatment of the disease. Sequences AAUSB3502 represent human colon specific protein antibody binding sites used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing, staging or monitoring colon cancer involves determining a colon specific gene in cells, tissues or body fluids in patient, and comparing it with levels of the gene from a normal human control.
                                                       .
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human colon specific polypeptide antibody binding site #31
                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; colon specific gene; CSG; cytostatic; metastasis; colon cancer staging; antibody binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.1%; Score 20; DB 5; Length 5; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels
Score 21; DB 2; I
Pred. No. 1.4e+06;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 21; 52pp; English.
                                                                                                                                                                                                                                                                                          AAU85454 standard; peptide; 5 AA
60.0%; Sccilarity 80.0%; Pre
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUL-2001; 2001WO-US022454.
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-171815/22.
Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macina RA, Sun Y;
                                                                                                       1 TOFTL 5
                                                                                                                                                         TDFVL S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-2002.
                                                                                                                                                                                                                                                                                                                                            AAU85454;
                                                                                                                                                                                                                                                                   AAU85454
                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                              Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
                                                                                                                                                                                                                                                                                                     The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, theumatoid arthritis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence corresponds to a peptide (CDR-H1-7; AAY14403) derived from the sequence of the heavy chain variable region complementarity determining region (CDR)-1 of the anti-hepatitis C virus (HCV) Ser/Thr protease monoclonal antibody (MAD) 8D4 protein. The peptide has a Tyr to Phe amino acid substitution at position 3 compared to the CDR-H1-7 peptide. The invention relates to the use of partial peptides (AAY14348-Y14353) from the MAD 8D4 for inhibiting HCV serine protease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neutralized antibody partial peptide derived from hepatitis C virus -
useful for inhibiting Hepatitis C Virus (HCV) serine protease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complementarity determining region; CDR; monoclonal antibody; MAb; hepatitis C virus; HCV; protease; binding site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide CDR-H1-7(Y3F) derived from anti-HCV protease MAb 8D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

74.3%; Score 26; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 0; Indels
                                                     Sablon E;
                                               Desmet J, Hufton S, Hoogenboom H,
                                                                                                                                                                                                                                                           Disclosure; Page 15; 68pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY14399 standard; peptide; 7 AA.
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Sequence 7 AA;

AAB30075;

12-OCT-2000

Synthetic.

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Sequences AAV40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a beta sheet. Peptides (AAY40601-C S4 peptide which forms part of a beta sheet. Peptides (AAY40601-C Y40609) together form a single-chain scaffold protein which contains at least 6 beta-strands. The scaffold protein which contains at least 6 beta-strands. The scaffold protein sconstructed of beta crands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands C furn two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. C form two beta sheets s1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each constructed of two beta sheets, with the structures of the next by manno acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold conduct cells. Therefore the scaffold protein may be used to target the complex to tumour cells. Another surface may be bound to a protein which binds to a surface may be bound to a cyctoxic molecule or an autoimmume antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target cumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used in catalizate individual peptides in a poptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines
                                                                                                                                                                                                                               New scaffold protein, useful for stabilizing antigens used as vaccines.
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SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
diabetic retinopathy; atherosclerosis.
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                                                                                                                                      Sablon
                                                                                                                                      Hoogenboom H,
                                                                                                                                                                                                                                                                              Disclosure, Page 6, 105pp, English.
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98EP-00870065
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                         (INNO-) INNOGENETICS NV.
                                                                                                                                      Desmet J, Hufton S,
                                                                                                                                                                                  WPI; 1999-542958/46.
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31-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
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                                                                                                                                                                                               Human, CTLA-4; scaffold protein, antigen-binding; receptor-binding;
SCA domain, cancer; thrombosis; osteoporosis, rheumatoid arthritis;
diabetic retinopathy; atherosqlerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.1%; Score 27; DB 3; Length 7; 83.3%; Pred. No. 1.4e+06; Live 1; Mismatches 0; Indels
                                                                                                                                                    Scaffold protein SCA S4 peptide SEQ ID NO: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sablon E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoogenboom H,
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              AAB30075 standard; peptide; 7 AA
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Best Local Similarity 83.3%,
                                                                                                        09-FEB-2001 (first entry)
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EP947582-A1 06-0CT-1999

Synthetic.

AAY40736;

RESULT 5

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Gaps

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AAY40737 standard; peptide; 7 AA

AAY40737

AAY40737;

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or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold may be bound to a protein which binds to a tumour antigen. This will target the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, CTLA-4; scaffold protein; antigen-binding; receptor-binding;
SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
diabetic retinopathy; atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                         85.7%; Score 30; DB 2; Length 7; 100.0%; Pred. No. 1.4e+06; cive 0; Mismatches 0; Indels
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AAB30076
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Sequences AAV40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAV40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheer. Peptides (AAV40601-CC V40609) together form a single-chain scaffold protein which contains at least 6 beta-strands. The scaffold protein which contains at least 6 beta-strands. The scaffold protein is constructed of beta strands also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands of the next by hydrogen bonds, which generate a beta sandwich architecture. The next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures of the next by hydrogen bonds, where at least one of the loops binds to a scaffold is constructed of two beta sheets, with the structures of the rule amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens or whole proteins such as receptors, or their fragments. It may be used to to bind two separate molecules. For example, one surface of the scaffold current which binds to a turnour antigen. Therefore the scaffold protein may be used to target the complex to tumour cells. Another surface may be bound to a protein which protein may also be used to charget chemotherapeutic agents to specific cells. It may also be used to diagnostic techniques, and to stabilize antigens used as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New scaffold protein, useful for stabilizing antigens used as vaccines.
                                                                                                                                                             Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine; tumour; chemotherapeutic agent.
                                                                                                                        84 derivative #11, beta strand of scaffold protein structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desmet J, Hufton S, Hoogenboom H, Sablon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 6; 105pp; English.
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Query Match
Best Local Similarity 83.30,
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77.1%; Score 27; DB 2; Length 7; 83.3%; Pred. No. 1.4e+06; ive 1; Mismatches 0; Indels

RESULT 4

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85.7%; Score 30; DB 3; Length 7; 100.0%; Pred. No. 1.4e+06; Live 0; Mismatches 0; Indels

Query Match Best Local Similarity 100. Matches 6; Conservative

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June 1, 2004, 10:40:31; Search time 45.6667 Seconds (without alignments) 43.310 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Perfect score:
Sequence:
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geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* A\_Geneseq\_29Jan04:\* .: geneseqp1980s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp1990s:\* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Aay40738 S4 deriva Aab30076 Scaffold Aay40737 S4 deriva Aab30075 Scaffold Transcrip
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Corticotr
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AUS pepti S4 deriva Scaffold Integrin AUS pepti Epitope t AUS epito Corticotr CRF2 non-Peptide C Epitope t Human col Description Aay40737 Aab30075 Aab30073 Aab30074 Aau85454 Aau85454 Aap82200 Aap82200 Aap82200 Aap82200 Aap82200 Aap85091 Aap85091 Aap85091 Aap85091 Aae13076 | Aam51422 | Aab97355 | Aae24897 | Ade65099 ( Ade51385 ( Aay52584 A Aay77708 Aab59859 Abg32853 | Add67264 | SUMMARIES AAY40738
AAB30076
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Abr55418 Amino aci Aaw75358 Hexapepti Aaw75290 Hexapepti	LFA-1 al Tryptic Peptide	Aag6484 Antihepat Abb5562 Mutated p Ab55651 Mutated p Aay51466 AAV VP3 d	Aab17215 IL-1 anta Aab52195 Human ant Abb72462 Interleuk Ade53380 FEN-1 rel	34 Strept 35 Strept 32 Epider	нев
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RESULT 1

Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine; tumour; chemotherapeutic agent. 84 derivative #12, beta strand of scaffold protein structure. AAY40738 standard; peptide; 7 AA 01-DEC-1999 (first entry) EP947582-A1. 06-OCT-1999. Synthetic. AAY40738; AAY 40738

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 AAY 40738

AAY 4

98EP-00870065 98EP-00870065 (INNO-) INNOGENETICS NV. 31-MAR-1998; 31-MAR-1998;

New scaffold protein, useful for stabilizing antigens used as vaccines. Disclosure; Page 6; 105pp; English.

Hoogenboom H, Sablon E;

Desmet J, Hufton S, WPI; 1999-542958/46. Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAX40607) which forms part of a scaffold protein. S4 is a beta serand peptide which forms part of a beta sheet. Peptides (AAX40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands and any also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands of contructed to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures calfold is constructed of two beta sheets, with the structures calfold is constructed of two beta strands are connected to other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens

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-1- MASS SPECTROMETRY: NW=596.6; METHOD=MALDI.
                                                                                                                                                                                                                                                                                                                                              0; Gaps
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Sperm attracting peptide SepSAP.
Sepim officinalis (Common cuttlefish).
Bukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
NCBL_TAXID=6610;
"A novel active pentapeptide from chicken brain identified by antibodies to FMRPamide.";
Nature 305:328-330(1983).
-!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
-!- SIMILARITY: BELONGS TO THE FARP (FMR.FAMIDE RELATED PEPTIDE)
FAMILY.
GO: GO:007218; P:neuropeptide signaling pathway; TAS.
Neuropeptide; Amidation.
MOD RES
5
SEQÜENCE 5 AA; 645 MW; 69D4073767400000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY, AND AMIDATION.
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PubMed=12207899;
Zatylny C., Marvin L., Gagnon J., Henry J.;
"Fertilization in Sepia officinalis: the first mollusk sperm-atracting peptide.";
Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
-!- PUNCTION: ATTRACTS SPERM INCREASING THE CHANCES OF GAMETE
                                                                                                                                                                                                                                                                                Query Match 17.1%; Score 6; DB 13; Length 5; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 1; Conservative 0; Mismatches 0; Indels
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6 AA; 597 MW; 72C8676AA0470000 CRC64;
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Q47029 Q47029;

RESULT 11

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Query Match

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"Characterization of the cmcH genes of Nocardia lactamdurans and Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem O-carbamoyltransferase for cephamycin biosynthesis."; Gene 162:21-27(1999)
Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
Liras P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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PubMed=6137771;
Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=86120353; PubMed=3003688; Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G. "Spinach plastid genes coding for initiation factor IF-1, ribosomal protein S11 and RNA polymerase alpha-subunit."; Mucleic Acids Res. 14:1029-1044(1986).

EMBL, X03496; CAA27215.1; --
GO; GO:0009507; C:chloroplast; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spinacia oleracea (Spinach).
Chloroplast.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Caryophyllales, Amaranthaceae, Spinacia.
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01-JUN-2002 (TrEWBLrel. 21, Created)
01-JUN-2002 (TrEWBLrel. 21, Last sequence update)
01-JUN-2003 (TrEWBLrel. 24, Last annotation update)
FMRPamide-like neuropeptide (LPLRF-amide).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b/f subunit IV (Fragment).
                                                                                                                                                   7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;
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7 AA; 907 MW; 644729D77409C420 CRC64;
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MEDILINE=94079349; PubMed=8257126;
Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;
"Analysis of the aac(3)-VIa gene encoding a novel 3-N-
                                                                                                                                                                                                                                                                                                                           Gaps
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Enterobacteriaceae; Enterobacter.
NCBI_TaxID=550;
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le+06;
ches 0; Indels
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                                                       88 kDa protein (Fragment).
Bacillus cereus
Bacteria; Firmicutes; Bacillales; Bacillus
NCBI_TaxID=1396;
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01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
AAD Al protein (Fragment).
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, Last sequence update)
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                                                                                                                                                                 STRAIN-NCIMB 11796;
Submitted (JUL-2001) to Swiss-Prot.
NON TER SA; 623 MW; 6B01AAA336F00000 CRC64;
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EMBL; M88012; AAA16193.1; -.
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les 1; Conservative 1; Mismatches
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SEQUENCE FROM N.A.
MEDLINE=96009872; PubMed=7557411;
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STRAIN=E;
MEDLINB=56427318; PubMed=8830682;
Rehm B.H.A., Ertesvag H., Valla S.;
Rehm B.H.A., Ertesvag H., Valla S.;
Rahm B.H.A., Ertesvag H., Valla S.;
Part of an alg gene cluster physically organized in a manner similar to that in Pseudomonas aeruginosa.";
J. Bacteriol. 178:5884-589(1996).
EMBL, X87973; CAA61230.1;
                                                                                                                                                                                                                                                                              STRAIN=DSM 20451;
PubMed=12112860;
Dress O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
Dress O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
Intigh pressure effects step-wise altered protein expression in Lactobacillus sanfranciscensis.";
Proteomics 2:765-774(2002).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN PROTEIN IS: 15 KDA.
NOW TER 1 1
NOW TER 6 6
SEQÜENCE 6 AA; 590 MW; 6DDD452D1AAC000 CRC64;
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                     01-UNA-2003 (TIEMBLR-1 24, Created)
01-UNA-2003 (TIEMBLR-1 24, Last sequence update)
01-UNA-2003 (TIEMBLR-1 24, Last sequence update)
UNKNOWN protein from 2D-page (Fragment)
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco)
Lactobacillus
Lactobacillus
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
AlgT protein (Fragment).
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Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 1; Conservative 1; Mismatches
                         6 AA
                       PRT;
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                       PRELIMINARY;
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
10 kDa cell wall protein (Fragment).
Nicotiana tabacum (Common tobacco).
Nicotiana tabacum (Common tobacco).
Spermatophyta; Nagmonliophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magmonliophyta; edulcotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
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STRAIN=4874;
MEDLINE=22056123; PubMed=12060770;
MEDLINE=22056123; PubMed=12060770;
Hoffmann D., Korn K., Selbig J.;
"Diversity and complexity of HIV-1 drug resistance: A bioinformatics approach to predicting phenotype from genotype.";
Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
EMBL; ARX3234411; -.
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Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
Wojtaszek P., Bolwell G.P.;
"Protecomic study of secondary cell wall proteins from transformed
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01-0CT-2002 (TrEMBirel. 22, Last sequence update)
01-0CT-2002 (TrEMBirel. 22, Last annotation update)
Truncated pol protein (Fragment)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: CELL WALL.
-i- TISSUE SPECIFICITY: XYLEM.
GO; GO:0005618; C:cell wall; IEA.
                                                              PRT;
                                                              PRELIMINARY;
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Matches 2; Conserv
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STRAIN=RF-1;
MEDLINE=9231861; PubMed=10217509;
MEDLINE=9231861; PubMed=10217509;
Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
"Organization and expression of nitrogen-fixation genes in the aerobic nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
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Bacteria; Cyanobacteria; Chroococcales; Cyanothece.
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Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
Sphingomonadaceae; Sphingomonas.
NCBI_TaxID=56193;
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
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7 AA; 868 MW; 71A452D1A699D460 CRC64;
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1; Mismatches
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01-JAN-1998 (TrEMBLrel. 05, Last sec
01-JUN-2003 (TrEMBLrel. 24, Last anz
Catechol-2,3-dioxygenase (Fragment)
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Microbiology 145:743-753(1999).
EMBL; AP003700; AAC35193.1; -.
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01-JUL-1997 (TrEMBLrel. 04,
01-JUL-1997 (TrEMBLrel. 04,
01-DEC-2001 (TrEMBLrel. 19,
Nifk (Fragment).
  2; Conservative
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MEDLINE=20011291; PubMed=10542330;
Pochling S., Piepersberg W., Wehmeier U.F.;
Pochling S., Piepersberg W., Wehmeier W.F.;
Nanalysis and regulation of the sec Y gene from Streptomyces griseus N2-3-11 and interaction of the SecY protein with the SecA protein.";
Biochim. Biophys. Acta 1447:298-302(1999).
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PubMeda-12112860;
Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
Drews O., Weiss W.;
High pressure effects steep-wise altered protein expression in Lactobacillus sanfranciscensis.";
Proteomics 2:765-774(2002).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN NOW_TER.
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Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Lactobacillus.
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Bacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1911;
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7 AA; 874 MW; 72D1A9DB5041A6F0 CRC64;
                                               Score 12; DB 5;
Pred. No. 1e+06;
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                                               Query Match 34.3%;
Best Local Similarity 66.7%;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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P8345 nicotiana t
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P70804 azotobacter
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70.488 Million cell updates/sec
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GenCore version 5.1 6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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### ALIGNMENTS

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WÓIBII.6.
Caenorhabditis elegans.
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                            "The sequence of C. elegans cosmid W01B11."; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilson R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AFO43704; AAO38592.1;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
1-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein W01B11.6.
                           7 AA.
                           PRT;
                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                               STRAIN-Bristol N2;
Bradshaw H., Graves T., Blair T.;
"The sequence of C. elegans cosmic
                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Bristol N2;
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                                                                                                                                                                                                                                              Wilson R.;
                                         Q7Z1C0;
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RESULT 1
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P83073 Q47029 P72081 O98866 P83308 P83569

P83533 P70804

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                                                                                                                                                                                                                                                                                                                                                                            TISSUBECErebral ganglion, and Thoracic ganglion, MEDLINE=98121193; PubMed=9461295; Duve H., Johhsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Carcinustatih 4.
Carcinus meenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca, Eumalacostraca, Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
NCBL TAXID=6759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cardinus maenas (Common shore crab) (Green crab).

Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Bumalacostraca; Bucarida; Decapoda; Pleocyemata; Brachyura;

Bubrachyura; Portunoidea; Portunidae; Carcinus.
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                                                                                                                   1; Indels
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22.9%; Score 8; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels
                                                                                          22.9%; Score 8; DB 1; Length 7; 66.7%; Pred. No. 1.40+05; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Cerebral ganglion, and Thoracic ganglion; MEDLINE=98121193; PubMed=9461295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALLS_CARMA STANDARD; PRT; 7 AA. P81808; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Carcinustatin 5.
                                                                                                                                                                                                                         7 AA.
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                                                                                             Query Match 22.9
Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                          STANDARD;
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P81807;
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RT allatostatin superfamily in the shore crab Carcinus maenas.";

RL Eur. J. Biochem. 250:727-734[1997].

CC -1- FUNCTION: May act as a neurcinsmitter or neuromodulator.

CC -1- SIMILARITY: Belongs to the allatostatin family.

KW Neuropeptide; Amidation; Multigene family.

FT MOD_RES 7 AA, 781 MW, 6728979CDCB476420 CRC64;

Query Match 22.9%; Score 8; DB 1; Length 7;

Best Local Similarity 66.7%; Pred. No. 1.46+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps
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Search completed: June 1, 2004, 11:16:49 Job time: 7.66667 secs

3 FTL 5

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Gaps

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-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
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-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SIMILARITY: Belongs to the allatostatin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
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Carcinus maenas (Common shore crab) (Green crab).

Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Bumalacostraca; Bucarida; Decapoda; Plocyemata; Brachyura;

Bubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carcinus maenas (Common shore crab) (Green crab).

Bukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca;

Bumlalcoeftraca; Bucarida, Decapoda, Plecyemata; Brachyura,

Bubrachyura, Portunoidea; Portunidae, Carcinus.
                                                                                      skin dorsal glands
                                                                                                                                                                                                                     22.9%; Score 8; DB 1; Length 5; 50.0%; Pred. No. 1.4e+05; rative 1; Mismatches 0; Indels
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                          Neuropeptide; Amidation; Multigene family.

MOD RES
7 7 AMIDATION (POTENTIAL)
SEQUENCE 7 AA; 770 MW; 672879CDCB5DDB70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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v 66.7%; Pred. No. 1...
0; Mismatches
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Best Local Similarity 50.0
Matches 1; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; asterids;
campanulids; Apiales; Apiaceae; Apioideae; Scandiceae; Daucinae;
                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last Sequence update)
16-OCT-2001 (Rel. 40, Last amotation update)
Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, AND MASS SPECTROMETRY.
TISSUB-Skin secretion;
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.,
"The structure of new peptides from the Australin red tree frog
Lincoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Secreted.
-!- PTM: Sulfation is important for activity and for the binding to putative membrane receptor (By similarity).
-!- SIMILARITY: Belongs to the phytosulfokine family.
Growth factor; Sulfation.
PRYTIDE 1
4 SULFATION.
MOD RES 1
3 SULFATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STOURNE, AND IDENTIFICATION BY MASS SPECTROMETRY.
STRAIN=cv. US-Harumakigosun;
MEDLINE=20212743; PubMed=10750705;
MEDLINE=20212743; PubMed=10750705;
Matsun H., Matsun T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
Kamada H., Sakagami Y.;
Kamada H., Sakagami Y.;
Fanda H., Sakagami Y.;
A secreted peptide growth factor, phytosulfokine, acting as a stimulatory factor of carrot somatic embryo formation.";
Plant Cell Physiol. 41:27-32(2000)
-!- FUNCTION: In presence of 2.4-D, stimulates proliferation of the cells, but does not stimulate differentiation into the somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Rubellidin 2.1.
Litoria rubella (Desert tree frog).
Elkaryota, Merasoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Pelodryadinae; Litoria.
NOBL TaxID=104895;
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3 3 SULFATION.
5 AA; 687 MW; 76C1BBS04B300000 CRC64;
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Matches 1; Conservative
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TEST LITRU
AC PE21 LITRU
AC PE2071;
DT 28-FEB-2003
DT 10-OCT-2003
DT 10-OCT-2003
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OC EUKATYOTA PER COC EVOLUTION R. T. T. LICOTA A COC EVOLUTION R. T. C. EVOLUTION R. T. C. EVOLUTION R. C. E
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SEQUENCE Query Match

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Gaps

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1; Indels

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SEQUENCE.
MEDLINE=87005522; PubMed=3093276;
MORI M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
White B.A., An F.Y., Clewell D.B., Suzuki A.;
"Isolation and structure of the Streptococcus faecalis sex pheromone,
                                                                                                                 01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0FB-1991 (Rel. 17, Last annotation update)
62x pheromone cAM373 (Clumping-inducing agent)
Enterococcus facetalis (Streptococcus facealis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NGBI_TAXID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR SPECIFICITY OF PHEROMONES TO PLASMIDS.
-!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
PIR; A25269; A25269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca, Eumalacostraca, Eucarida, Decapoda, Pleccyemata, Brachyura, Bubrachyura, Portunoidea, Portunidae, Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                     FEBS Lett. 206:69-72 (1986).
-!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
HARBORING PAM373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Carcinustatin 14.
Carcinus maenas (Common shore crab) (Green crab).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 22.9%; Score 8; DB 1; Le
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1;
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                                                                                                             STANDARD;
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Best Local Similarity
2; Conserva
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P81817;
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                                                                                                               CIA ENTFA P11932;
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                                                                         RESULT 8
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Enterococcus faccalis (Streptococcus faccalis).
Bacteria, Firmicutes, Lactobacillales, Enterococcaceae, Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE=899008313; PubMed=3139658;
Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
Mori M., Sakagiu J.C., Dumny G.M., Suzuki A.;
"Structure of cofflo, a peptide sex pheromone which induces
conjugative transfer of the Streptococcus faecalis tetracycline
resistance plaemid, pCF10.";
J. Biol. Chem. 263:14574-14578(1988).
-!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
HEMOLYSIN PLASMID PCF10.
                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Skin secretion;
whitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog
"Peptides from the Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                   Electrin 4.
Litoria rubella (Desert tree frog).
Litoria rubella (Desert tree frog).
Amphibia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia: Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
NCBL TaxID=104895;
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28.6%; Score 10; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.46+05;
Matches 1; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.7%; Score 9; DB 1; Length 7; 100.0%; Pred. No. 1.40+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AA; 790 MW; 72C9D2C731B2C740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amphibian defense peptide; Amidation.
MOD RES 5 AMIDATION.
SEQUENCE 5 AA; 616 MW; 61F2DIA059A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                         S AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Skin.
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Best Local Similarity 100.0
Matches 2; Conservative
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CCF1\_ENTFA RESULT 7

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Wabritz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                  Litoria rubella (Desert tree frog).
Estaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Litoria rubella (Desert tree frog).
Butaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae; Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Skin secretion,
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao.C.,
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao.C.,
Tyler M.J., Wallace J.C.,
"The structure of new peptides from the Australin red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the st
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:555-563 [1966].
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aust. J. Chem. 52:639-645(1999).
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Expressed by the skin dorsal glands.
Amphibian defense peptide.
SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLUTAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-!- MASS SPECIROMETRY: MW=655; NETHOD=FAB.
Amphibian defense peptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.4%; Score 11; DB 1; Length 5; 100.0%; Pred. No. 1.4e+05; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AA; 656 MW; 71A9C9CB10300000 CRC64;
                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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28-FEB-2003 (Rel. 41, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Rubellidin 3.2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, AND MASS SPECTROMETRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=104895;
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                                                                                                    RESULT 4

RE31_LITRU
AC P82072;
DT 28-FEB-2003
DT 28-FEB-2003
DT 0-OCT-2003
DT 0-OCT-2
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ID RE32 LITRU
AC P82073;
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-!- PATHWAY: Biotin biosynthesis.
-!- SUBUNIT: Homodimer.
-!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=89006280; PubMed=2971595;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
Citrobacter freundil and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
-!- CATALYTIC ACTIVITY: S.adenosyl-L.methionine + 8-amino-7-
oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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01-07N-1990 (Rel. 13, Last sequence update)
01-07N-1990 (Rel. 140, Last ennotation update)
Adenosylmethionine-8-amino-7-oxonomanoate aminotransferase
(RC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Citrobacter.
NCBI_TaxID=546;
Aust. J. Chem. 49:955-963(1996).
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                      -!- SUBCELLUIAR LOCATION: Secreted.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-!- MASS SPECIFOMETRY: MW=598; METHOD=FAB.
Amphibian defense pepty (SPECIFICATION)
SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                    34.3%; Score 12; DB 1; Length 5; 100.0%; Pred. No. 1.4e+05; tive 0; Mismatches 0; Indels
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PROSITE; PS00600; AA TRANSFER CLASS 1; PARTIAL.
Biotin biosynthesis; Transferase; Aminotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AA; 582 MW; GAAABIBIA6F00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AA.
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EMBL; M21922; -; NOT\_ANNOTATED\_CDS PIR; 140697; 140697.

Pyridoxal phosphate.

NON TER SEQUENCE

aminotransferases.

diaminononanoate.

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Query Match Best Local Similarity Matches 2; Conserv

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BIOA CITFR P13071;

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Query Match Best Local Similarity Matches 2; Conserv

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(EC 2.6.1.62) (7,8-diamino-p aminotransferase) (Fragment)

Citrobacter freundii.

SEQUENCE FROM N.A.

Gaps

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anthopleura

litoria rub artioposthi pardachirus acheta dome canis famil escherichia zea mays (m

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ALIGNMENTS

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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
Rubellidin 1.1.
Litoria rubella (Desert tree frog).
Lataryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Larva;
MEDLINE-98054539; PubMed-9332829;
MEDLINE-98054539; PubMed-9332829;
MEDLINE-98054539; PubMed-932829;
Dave H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A. There allatostatin superfamily.";
Peptides 18:1301-1309(1997).
Induropeptide; Amidation.
MOD_RES
7 A., 873 MW; 672879CABB569350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Skin secretion, Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C., Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C., P.C., Warner S.T., Wabnitz S.T., Wabnitz S.T., Wann peptide profile as a probe for the fore evolutionary trends of amphibians.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cydia pomonella (Codling moth).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAS-2001 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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P82070;
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P82158;
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RESULT 1
REIL LITRU

AC PREOTO
DT 28-FEB
DT 10-OCT
DE RUBELL
OC BUKARY
OC AMBRID
OC AMBRID
OC AMBRID
OC ARRAY
CO AMBRID
OC ARRAY
CO AMBRID
OC TISSUE
RR 1715
RR 574
RR 574
RR 774
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RT 11100
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P82072 litoria rub
P82073 litoria rub
P820100 litoria rub
P810103 enterococcu
P11932 enterococcu
P81817 carcinus ma
P8261 daucus carc
P82071 litoria rub
P81805 carcinus ma
P81806 carcinus ma
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2004, Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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ALL3_CARMA
ALL3_CA
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Maximum Match 100%
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C)Accession: A6096
R;Broom, M.F.; Mellor, D.M.; Chadwick, V.S.
Experientia 45, 1097-1099, 1989
A;Title: Purification and amino acid sequencing of naturally occurring N-formyl-methiony A;Reference number: A60986; MuID:90092408; PMID:2689204
A;Accession: A60986
A;Molecule type: protein
A;Residues: 1-6 <BRO>
C;Comment: This hexapeptide was the longest of several N-formyl oligopeptides reported.
F;1/Modified site: N-formylmethionine #status experimental
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C.Species: Escherichia coli
C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
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A,Reference number: S69237; MUID:95139068; PMID:7837271
A;Accession: S69237
A;Molecule type: protein
A;Residues: 1-5 - PETS-
A;Experimental source: strain F1, DSM 3639
C;Keywords: cell wall; glycoprotein; heat-stable protein
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Job time : 11.6667 secs
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C;Species: Staphylothermus marinus
C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C;Accession: S69237
C;Accession: S69237
C;Accession: S6924
D; Nitsch, M; Kuehlmorgen, B; Golbik, R; Lupas, A; Kellermann, J; E
J; Mol. Biol. 245, 385-401, 1995
A;Title: Tetrabrachion: a filamentous archaebacterial surface protein assembly of u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   blood cell protein B - Ascidia ceratodes (fragment)
NyAlternate names: Abcp-B
NyAlternate names: Abcp-B
C;Species: Ascidia ceratodes
C;Species: Ascidia ceratodes
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jun-1999
C;Accession: S6832
M.M.; Waite, J.H.
Arch. Biochem. Biophys. 324, 228-240, 1995
A;Title: Novel 3, 4-di- and 3, 4,5-trihydroxyphenylalanine-containing polypeptides fr
A;Reference number: S68325; MUID:96132650; PMID:8554314
                                                                                                                                                                                                                                                                                                                                                                                                                                               major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: E60274 # H.G.; Harboe, M.; Kinomoto, M.
R;Nagal, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the A;Reference number: A60274; MUID:91099889; PMID:1898899
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A,Realdues: 1-5 <TAT>
F;2/Modified site: 3',4' 5'-trihydroxyphenylalanine (Tyr) #status experimental
F;4/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental
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                                                                                                                                         DB 2; Length 5; 2.8e+05;
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Best Local Similarity 100.0%; Pred. No. 2.8
Matches 2; Conservative 0; Mismatches
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     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 < VOG>
A;Cross-references: GB:M62408
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A,Molecule type: protein
A,Residues: 1-5 <NAG>
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2 YPIT 5
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Cytochrome-C oxidase (EC 1.9.3.1) chain I [imported] - river lamprey)
Cytochrome-C is in the condition Lampetra fluviatilis (river lamprey)
Cytochesion: T13892
A.Pitle: Tab main features of the craniate mitochondrial DNA between the NDI and the COI A.Reference number: Z17775; MUID: 97398704; PMID: 9254918
A.Accession: T13892
A.Accession: T13892
A.Accession: T13892
A.Residues: 1-3 - DEL-
A.Molecule type: DNA
A.Residues: 1-3 - DEL-
A.Coross-references: EMBL:Y09528; NID: 92340016; PIDN: CAA70721.1; PID: 94379123
A.Genemics: mitochondrion
A.Note: COI
Cytochecic COI
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C;Species: 24-Uul-1992 #text_change 30-Sep-1993
C;Accession: E42364
R;Yogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
J; Bacteriol. 173, 3564-3572, 1991
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seq
A;Reference number: A42364; MUID:91288342; PMID:1646201
                                                                                                                                                                                                                                                                                            globulin IV alpha subunit delta-1 chain, seed - cucurbit (fragments)
N.Alternate names: 11S globulin alpha subunit delta-1 chain
C.Species: Cucurbita sp. (cucurbit)
C.Species: Cucurbita sp. (cucurbit)
C.Species: Clavov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
C.Accession: 80966
C.Accession: 80966
A.Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and A.Reference number: 809066
A.Reference number: S09066
A.Rocession: 809066
A.Rocession: 809066
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     Length
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Score 10; DB 2; L
Pred. No. 2.8e+05;
1; Mismatches 1;
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50.0%; Pred. No. 2.8e+05;
iive 1; Mismatches 1;
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Best Local Similarity 50.0%;
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity 100.
Matches 2; Conservative
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Diotin A - Citrobacter freundii (fragment)
C;Species: Ctrrobacter freundii
C;Species: Ctrrobacter freundii
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C;Accession: 140697
G;Shiuan, D:; Campbell, A.
Gene 67, 203-211, 1988
A;Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citr
A;Reference number: 140697; WUD: 89006280; PMID: 2971595
A;Accession: 140697
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Melecule type: DNA
A;Residues: 1-4 <RES>
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C;Species: Mus musculus (house mouse)
C;Date: 1-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0650
R;Feeney, A.J
B.Xp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain V-III region (Gag) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1899 #sequence_revision 29-Jun-1889 #text_change 16-Aug-1996
C;Accession: E30668
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, A. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM A;Reference number: A30601; MUID:89215279; PMID:2496160
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A;Molecule type: mRNA
A;Residues: 1-6 <FEB>
A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
31.4%; Score 11; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.4%; Score 11; DB 2; I 40.0%; Pred. No. 2.8e+05; tive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <GON>
C;Reywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: M21922; NID: 9144434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 40.0
Matches 2; Conservative
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                          2 DF 3
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J. Exp. Med. 174, 115-124, 1991

A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A.Recession: PT0644

A.Scaession: PT0644

A.Necelecule type: mRNA
A.Mesidues: 1-5 < PES>
A.Residues: 1-5 < PES>
A.Experimental source: newborn thymus, strain BALB/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A.Titler. Juncitional sequences of fetal T cell receptor beta chains have few N regions.
A.Reference number: PT0509; MUID:91277601; PMID:1711558
A.Accession: PT0665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment) (Systeties: Escherichia coli (C.Species: Escherichia coli (C.Species: Bacherichia coli (C.Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 08-Oct-1999 (S.Accession: B39127 B.Hardesty, C.; Ferran, C.; DiRienzo, J.M. Bacteriol. 173, 449-456, 1991 AjTitle: Plasmid-mediated sucrose metabolism in Bscherichia coli: characterization of
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                       T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1392 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0644
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.3%; Score 12; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5;
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A;Molecule type: mRNA
A;Rosidues: 1-7 <FEED.
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A39127; MUID:91100329; PMID:1846143
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 34.3%; Score 12; DB 2; L Best Local Similarity 50.0%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: B39127
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-7 <HAR>
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2 SSFT 5
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RESULT 3
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GenCore version 5.1.6
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June 1, 2004, 10:56:46; Search time 11.6667 Seconds (without alignments) 57.715 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-712-819C-5 35 1 TDFTLTI 7 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapext 0.5

283366 seqs, 96191526 residues Searched:

457 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	pev-kinin 2 - pena	ini	T-cell receptor be	ansfera	T-cell receptor be	biotin A - Čitroba	Iq kappa chain V-I	elî're	qlobulin IV alpha	cytochrome-c oxida	flagellar protein	major protein anti	blood cell protein	e pro	N-formyl oligopept	hypothetical prote	28K ubiquitin-immu	Y protein - human	MHC H2-L antigen -	T-cell receptor be	Na+/K+-exchanging	pilE protein - Esc	oheromone c	sex pheromone CCF1	il recepto	-cell receptor	ribosomal protein	ribosomal protein	_
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تب وہ	37.1	34.3	34.3			31.4		28.6	28.6		25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	ď.	ď	22.9	22.9
Score	13	12	12	12	12	11	11	10	10	o,	σn	σ'n	σ'n	σ	σ	60	თ	on	σ	0	ق	σı	თ	σı	on.	60	80	∞	œ
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fulicin - giant Af	м	T-cell receptor be	27.5 kda structura	27.5K structural p	27.5K structural p	28.5K structural p	28K structural pro	phytosulfokine alp	transferrin - bovi	Fc epsilon RIIb -	T-cell receptor be	T-cell receptor be	seed protein ws-5	18K protein 5507 -	T-cell receptor be
A44692	PT0729	PT0590	G44817	144817	E44817	C44817	A44817	JT0870	A19780	A46474	PT0637	PT0641	E61491	PS0254	PT0642
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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1 PD0028  DP0V-Kinin 2 - penaeid shrimp (Penaeus vannamei) (fragment) C;Species: Penaeus vannamei C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 19-May-2000 C;Accession: PD0028 R:Nieto, J: Veelaert, D:; Derua, R:; Waelkens, E:; Cerstiaens, A.; Coast, G.; Devr Biochem. Biophys. Res. Commun. 248, 406-411, 1998 A;Title: Identification of one tachykinin- and two kinin-related peptides in the bi A;Reference number: PD002; MUID:98342103; PMID:9675150 A;Reference number: potetin A;Reference number: protetin A;Reference number:	PB 1 DFS 3  RESULT 2 A32516 cholecystokinin-5 - dog Chocerstokinin-5 - dog N:Alternate names: CCK-5 C;Species: Canis lupus familiaris (dog) C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000 C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000 C;Date: 10-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000 R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, Am.;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and A;Reference number: A32516; MUID:87153871; PMID:3826354 A;Molecule type: protein A;Residues: 1-5 cSHI> C;Comment: This peptide corresponds to the five carboxyl-terminal residues of chole C;Superfamily: gastrin C;Superfamily: gastrin C;Superfamily: gastrin C;Keywords: amidated carboxyl end; neuropeptide F;S/Modified site: amidated carboxyl end (Phe) #status experimental	Query Match 34.3%; Score 12; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Gaps
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US-08-388-653-46

; Sequence 46, Application US/08388653
; Patent No. 5869337
; GENERAL INFORMATION:
; APPLICANT: Crabiner, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Mandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: GENERAL DOTHER BIOLOGICAL BVENTS;
INUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
ADDRESSEE: ALAD PHARMACCULICALS, INC.
; STREET: 26 Landsdowne Street
CITY: Cambridge
STATE: Massachusetts
COUTRY: USA
                                                                                                                                Score 16; DB 2; Length 6; Pred. No. 3e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
50.0%; Score 16; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: ACTORIN: PC/DOS/MS/DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,653
FILING DATE: 14-FEB-1995
CLASSIFICATION NUMBER: US 08/478,386
FILING DATE: O7-UJU-1995
ATTORNEY/AGENT INFORMATION:
NAME: Figg, E. Anthony
RESERRENCE/DOCKET NUMBER: 2054-114A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: June 1, 2004, 11:20:17
Job time : 14.6667 secs
                                                                                                                             Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
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TELEFAX: (202) 783-6031
INFORMATION FOR SEG ID NO: «
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                ; MOLECULE TYPE: protein US-08-292-597-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-388-653-46
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STATE: Massachusetts
ZIP: 02139
ZIP: 02139
COMPUTEX: USA
ZIP: 02139
COMPUTER: FLOADY disk
COMPUTER: IBM PC Compatible
OPERATIO SYSTEM: PC/DOS/MS/DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292.597
FILING DATE: 18/AuG/1994
APPLICATION NUMBER: 23
FILING DATE: 18/AuG/1994
APPLICATION NUMBER: 27.195
RIGHSTRATION NUMBER: 27.195
REFERENCE/DOCKET NUMBER:
OPERATING SYSTEM: PC/DOS/MS/DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,386A
FILING DATE: 07/JUN/1995
CLESSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Figg, E. Anthony
REGISTRATION NUMBER: 2054-114A
REPREMENCE/DOCKET NUMBER: 2054-114A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-601
INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acide
TYPE: amino acide
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US-08-292-597-46
Sequence 46, Application US/08292597
Sequence 46, Application US/08292597
PAPLICANT: Gerald R. Crabtree
APPLICANT: Schreiber, Stuart L.
APPLICANT: Spener, David M.
APPLICANT: Wandless, Thomas J.
APPLICANT: Wandless, Thomas J.
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD PHARMACCULICALS, INC.
STREET: 26 Landsdowne Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-478-386A-46
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us-09-712-819c-1.closed.rai

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APPLICANT: Crabtree, Gerald R.
APPLICANT: Schreiber, Stuart L.
APPLICANT: Schreiber, Stuart L.
APPLICANT: Wandless, Thomas J.
APPLICANT: Wandless, Thomas J.
APPLICANT: Belabaw, Peter
IITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
CORRESPONDENCES. 81
CORRESPONDENCE ADDRESS:
ADDRESSEE ARIAD PHARMACCULICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%; Score 16; DB 1; Length 6; 60.0%; Pred. No. 3e+05;
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Deficition, Mike
APPLICANT: Hefferian, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: BRESKIN & PARR
STREET: 40 King Street Weet
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSH 3Y2
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1:0, Version #1:30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION: 536
CURRENT APPLICATION BATA:
APPLICATION: 536
CURRENT APPLICATION STATE
CURRENT APPLICATION S
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STRET: 26 Landsdowne Street
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFO 5740

NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEPHONE: (416) 361-1398
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.0
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:|:
2 LTLSN 6
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US-08-478-386A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-252-995D-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Park, John E.
APPLICANT: Park, John E.
APPLICANT: Bamberger, Uwe
APPLICANT: Bamberger, Uwe
APPLICANT: Banderger, Uwe
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgengific Antibody with Improved Producibility
TITLE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT APPLICATION NUMBER: EP 98107925.4
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER PILING DATE: 1998-04-30
SARLIER PILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Ver. 2.0
SEG ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                      GENERAL INFORMATION:
APPLICANT: Sandlie, Inger
APPLICANT: Sandlie, Inger
APPLICANT: Bogen, Bjarne
TATLE OF INVENTION: A Modified Immunoglobulin Molecule
TITLE OF INVENTION: Incorporating an Antigen in a No. 6294654-CDR
TITLE OF INVENTION: Loop Region
TITLE OF INVENTION: Loop Region
TITLE OF INVENTION: Loop Region
TITLE OF INVENTION WHERE: US/08/860,904
CURRENT FILING DATE: 1997-09-29
BARLIER APPLICATION NUMBER: US/08/60116
BARLIER APPLICATION NUMBER: GB 9501079.9
FARLIER FILING DATE: 1995-01-19
SARLIER PILING DATE: 1995-01-19
SARLIER FILING DATE: 1995-01-19
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16; DB 3; Length 4;
Pred. No. 3e+05;
1; Mismatches 0; Indels
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Pred. No. 3e+05;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 47, Application US/09301593A Patent No. 6455677 GENERAL INFORMATION:
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                                     Sequence 9, Application US/08860904
Patent No. 6294654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM; Mus sp.
US-08-860-904-9
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Parent No. 6610506
GENERAL INFORMATION:
APPLICANT: Lo. Reggie Y.C.
APPLICANT: Lo. Reggie Y.C.
APPLICANT: BCATYVETS, Anthony B.
APPLICANT: POTTER, Andrew A.
TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
TITLE OF INVENTION: PASTEURER: US/08/753,750B
CURRENT APPLICATION NUMBER: CA 2,164,274
PRIOR FILING DATE: 1995-112-01
PRIOR FILING DATE: 1995-12-01
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
ILENGTH: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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            CITY: TALAWALLE COUNTY:

STATE: Wisconsin
COUNTRY: U.S.A.

ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,401A
APPLICATION NUMBER: US/08/739,401A
APPLICATION NUMBER: 35,433
ATTORNEY/AGENT INFORMATION:
NAME: BAKET, Jean C.
REGISTRATION NUMBER: 35,433
REPERENCE/DOCKET NUMBER: 35,433
REPERENCE/DOCKET NUMBER: 35,433
RELEPAR. (414) 277-5709
TELEPAR: (414) 277-5709
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Pred. No. 3e+05;
1; Mismatches
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33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Escherichia coli
US-08-753-750B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 33.3
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
          Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TLTISS 7
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2 TITVTA 7
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US-08-753-750B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-739-401A-6
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APPLICANT: Unilever PLC
TITLE OF INVENTION: New products comprising inactivated yeasts or moulds
TITLE OF INVENTION: New products comprising inactivated yeasts or moulds
TITLE OF INVENTION: Derovided with active antibodies
FILE REFERENCE: t-7055
CURRENT APPLICATION NUMBER: US/09/266,805
CURRENT FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 5
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-09-530-139-14
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Batent No. 587461
GENERAL INFORMATION:
APPLICANT: Neitz, Maureen B.
APPLICANT: Neitz, Marren B.
TITLE OF INVENTION: DEFECTION OF CONE-PHOTORECEPTOR-BASED
TITLE OF INVENTION: VISION DISORDERS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Quartles & Brady
STREET: 411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FALCHLIA NO. 96.70453

GENERAL INCORMATION:
APPLICANT: FRENKEN, LEON GERARDUS
APPLICANT: HOWELL, STEVEN
APPLICANT: HOWELL, STEVEN
APPLICANT: HOWELL, STEVEN
TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
FILE REPERENCE: 60113/269075/ASH
CURRENT APPLICATION NUMBER: US/09/530,139
CURRENT FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/EP98/06991
PRIOR PLLING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 77
SEQ ID NOS: 77
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                        Score 17; DB 4; Length 6;
Pred. No. 3e+05;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/09530139 Patent No. 6670453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                        Query Match 53.1
Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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2 VTVSS 6
                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: llama
US-09-266-805-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-09-530-139-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-08-739-401A-6
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APPLICANT: Boulanger, Flerre
APPLICANT: Boulanger, Plerre
APPLICANT: Boulanger, Saw See
APPLICANT: Boulanger, Lucie
APPLICANT: Boulanger, Lucie
TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
FILE REPRENCE: 032751-036
CURRENT APPLICATION NUMBER: US/09/155,613A
CURRENT APPLICATION NUMBER: PCT/FR98/00184
PRIOR FILING DATE: 1997-01-30
PRIOR PELING DATE: 1997-01-30
PRIOR PELING DATE: 1997-01-30
PRIOR PELING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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4; Conservative 0; Mismatches 0; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,177
FILING DATE: 27-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17; DB 4;
Pred. No. 3e+05;
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                                                                FILING DATE: 27-NOV-1996
CLASSIFICATION: 435
ATTONNEY, AGENT INFORMATION:
NAME: BECKEY, Cheryl L.
REGISTRATION NUMBER: 35,441
REPERENCE/DOCKET NUMBER: 6004.US.01
TELECHONE: 847-935-1729
TELEPHONE: 847-935-1729
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 59, Application US/09155613A Patent No. 6420120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-757-177-16
                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
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US-09-266-805-5
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Patent No. 656996

Patent No. 656996

Patent No. 656996

APPLICANT: Blaschuk, Orest W.

APPLICANT: Branchuk, Orest W.

APPLICANT: Symonda, James Matthew

APPLICANT: Gymonda, James Matthew

APPLICANT: Gymonda, James Matthew

APPLICANT: Gymonda, James Matthew

APPLICANT: Gymonda, James Matthew

TITLE OF INVENTION: CAMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: CAMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

CURRENT APPLICATION NUMBER: US/09/839,542B

CURRENT FILING DARE: 2001-04-20

NUMBER OF SEQ ID NOS: 4052.
                                                                      OTHER INFORMATION: Representative linear modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion JOTHER INFORMATION: recognition sequence US-09-187-859-637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Representative linear modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion OTHER INFORMATION: recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MUCRELI, PRADIP
APPLICANT: HARDS, ROBERT G.
APPLICANT: HARDS, ROBERT G.
APPLICANT: HARDS, ROBERT G.
APPLICANT: HURWOND, JENNIFER M.
APPLICANT: LEGNARD, AMANDA EUN-YEONG
TITLE OF INVENTION: METHODS OF PRODUCING A RECOMBINANT PROTEIN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park Sad
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                          Query Match 56.2%; Score 18; DB 4; Length 7; Best Local Similarity 57.1%; Pred. No. 3e+05; Matches 4; Conservative 1; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08757177 Patent No. 6071718 GENERAL INFORMATION:
  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                             1 FTLTISS 7
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US-09-839-542B-637
                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-839-542B-637
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US-08-757-177-16
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                                                   FEATURE:
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GENERAL INFORMATION:
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Sequence 20. Application US/08753750B

Patent No. 6610506

GENERAL INPORMATION

APPLICANT: Control Schryvers, Anthony B.

APPLICANT: Potter. Andrew A.

TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME

TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME

TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME

TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME

TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME

CURRENT APPLICATION NUMBER: US 0.05

PRIOR FILING DATE: 1996-11-29

PRIOR FILING DATE: 1995-12-01

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 20
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| Patent No. 6158920
| GENERAL INFORMATION:
| APPLICANT: Blaschuk, Orest W. APPLICANT: Gour, Barbara J. TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
| TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
| TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
| FILE REFERENCE: 100086.407C1 | CURRENT FILING DATE: 1998-11-06 | NUMBER OF SEQ ID NOS: 4052 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NO 637 | LENGTH: 7
                                                                                           Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                   Sequence
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US-08-177-109A-7
US-08-68-7
US-09-040-216-28
US-08-65-743B-63
US-08-65-701-22
US-09-040-216-55
US-08-591-632-17
US-08-591-632-23
US-08-591-632-23
US-09-611-451-17
US-09-611-451-23
US-09-611-451-23
US-09-611-451-23
US-08-297-731-4
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Best Local Similarity 42.9%;
Matches 3; Conservative 3
         TYPE: PRT
ORGANISM: Escherichia coli
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US-09-187-859-637
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Sequence 637, App
Sequence 637, Appl
Sequence 59, Appl
Sequence 5, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 46, Appl
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                                                                                                                                                                                                         June 1, 2004, 11:13:51; Search time 13.6667 Seconds (without alignments) 26.443 Million cell updates/sec
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2: /cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-187-859-637

US-09-183-637

US-09-155-613A-59

US-09-556-805-5

US-09-530-139-14

US-08-753-750B-19

US-08-753-750B-19

US-08-753-750B-19

US-08-753-750B-19

US-08-252-995D-7

US-08-252-995D-7

US-08-288-63-46

US-08-288-63-46

US-08-288-63-46

US-08-288-63-46

US-08-288-63-46

US-08-283-888-46

US-08-283-888-46

US-09-157-753-46

US-09-157-753-46
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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32
1 FTLTISS 7
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Match Length
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Perfect score:
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Search completed: June 1, 2004, 11:31:22
Job time : 35.6667 secs
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| Publication No. US20030190311A1 |
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT: DALL'ACQUA, WILLIAM |
| APPLICANT: WARD, ELIZABETH SALLY |
| APPLICANT: WARD, ELIZABETH SALLY |
| TITLE OF INVENTION HOWER: US/10/020,354 |
| CURRENT FILING DATE: 2001-12-12 |
| PRIOR PILICATION NUMBER: 60/234,884 |
| PRIOR FILING DATE: 2000-12-12 |
| PRIOR FILING DATE: 2001-02-09 |
| WINBER OF SEQ ID NOS: 118 |
| SOUTWARE PARENT OF 118 |
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APPLICANT: Bark, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Leger, Oliver
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Retig, Wolfers Berig, Wolfer W.
APPLICANT: Retig, Wolfer W.
APPLICANT: Retig, Wolfer W.
APPLICANT: Retig, Wolfer: US 09/301,59,006
CURRENT APPLICATION NUMBER: US 09/301,593
PRIOR APPLICATION NUMBER: US 09/301,593
PRIOR PILING DATE: 1999-04-29
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PARENTIN VET. 2.0
SEQ ID NO 47
            Gaps
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        1; Indels
0; Mismatches
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Sequence 47, Application US/10159006

Publication No. US20030143229A1
4; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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; ORGANISM: Homo sapiens
US-10-159-006-47
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ORGANISM: Homo sapiens
                                                                             3 LTISS 7
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US-10-020-354-102
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Matches
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GENERAL INFORMATION:
APPLICANT: Boulanger, Pierre
APPLICANT: Boulanger, Pierre
APPLICANT: Boulanger, Pierre
APPLICANT: Hong, Saw See
APPLICANT: Hong, Saw See
TITLE CONTRIBUTION: Use of a Polypeptide as Cell Receptor for Adenoviruses;
FILE REFERENCE: 032751-036
CURRENT APPLICATION NUMBER: US/10/156,820
CURRENT FILING DATE: 1998-01.30
PRIOR APPLICATION NUMBER: FR 97/01005
PRIOR PRILING DATE: 1997-01-30
FRIOR PILING DATE: 1997-01-30
FRIOR PILING DATE: 1997-01-30
FRIOR FILING DATE: 1997-01-30
Gaps
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Sequence 97, Application US/10097175
Publication No. US20030045680A1
Publication No. US20030045680A1
APPLICANT: JOYAL, JOHN L.
APPLICANT: MUELLER, JOHN L.
APPLICANT: GZA, VIBHA B.
APPLICANT: FINDEIS, MARK A.
TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR FILE REFERENCE: PPI-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 6;
1e+06;
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, OTHER INFORMATION: Androgen Receptor Binding Polypeptides US-10-097-175-97
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80.0%; Pred. No. 1e+06;
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Pred. No. 1e+0
1; Mismatches
  Mismatches
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CURRENT FILING DATE: 2002-03-12
CURRENT FILING DATE: 2002-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR PRILING DATE: 2001-03-12
PRIOR FILING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 97
LENGTH: 6
                                                                                                                                                                            RESULT 12
18-10-156-820-59
Sequence 59, Application US/10156820
Publication No. US20020150558A1
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Best Local Similarity 75.0%;
Matches 3; Conservative
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ORGANISM: Artificial Sequence
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  4; Conservative
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Best Local Similarity
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Publication NO. US20040067523A1
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: MERULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/698,489
CURRENT FILING DATE: 2003-11-03
PRIOR APPLICATION NUMBER: US Assigned
PRIOR FILING DATE: 2003-11-03
PRIOR APPLICATION NUMBER: 09/777,921
PRIOR APPLICATION NUMBER: 09/777,921
NUMBER OF SEC ID NOS: 126
SOFTWARE: FastSEQ for Windows Version 4.0
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                   53.1%; Score 17; DB 9; Length 6; llarity 100.0%; Pred. No. 16+06; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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US-10-698-489-17
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Best Local Similarity
                         Query Match
Best Local Similarity
Matches 4; Conserv
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2 VTVSS 6
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Sequence 17, Application US/09777921A
Fatent No. US202011513641
GENERAL INFORMATION:
FATENT NO. US202011513641
FATENT NO. US2020201513641
FITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO1103
CURRENT APPLICATION UNMERS: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SEQ ID NO 17
LENGTHARE: FREESEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 6
TYPE: PRT
TYPE: PRT
CRAMISM: Homo sapiens
US-09-777-921A-17
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                           Muyldermans, Serge
TITLE OF INVENTION: VARIABLE FRAGMENTS OF IMMUNOGLOBULINS -
USE FOR THERAPEUTIC OR VETERINARY PURPOSES
                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: SPENCER & FRANK
STRET: 1100 New York Avenue, N.W., Suite 300 East
CITY Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC compatible

COMPUTER: ISM PC compatible

CORFWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/154,971

FILING DATE: 28-MAY-2002

CLASSIFCATION: «Unknown»

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/945,244
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APPLICATION NUMBER: PCT/EP96/01725
FILING DATE: 25-APR-1996
APPLICATION NUMBER: EP 95400932.0
FILING DATE: 25-APR-1995
ATTORNEY/AGBNT INFORMATION:
NAME: Gollin, Michael A.
REGISTRATION NUMBER: 31,957
REPERSONGYIOKET NUMBER: GUPLA 0003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: <Unknown>
APPLICANT: Hamers, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 29
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Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                          NUMBER OF SEQUENCES:
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| Publication No. US2030036093A1
| Publication No. US2030036093A1
| APPLICANT: Floudas, Christopher A. APPLICANT: Rlepeis, John L. APPLICANT: Rlepeis, John L. TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and TITLE OF INVENTION: Polypeptide Tertiary Structures
| FILE REPERNOE: PU-0007 | Publication Vivial Application Vivial Application
                                                                                                                                                                                                                                                                                                             US-05-78
US-05-107
US-05-107
Sequence 107, Application US/09788006
Sequence 107, Application US/09381
GENERAL INFORMATION:
APPLICANT: Floudas, Christopher A.
APPLICANT: Floudas, Christopher A.
TITLE OF INVENTION: Polypeptide Tertiary Structures
TITLE OF INVENTION: Polypeptide Tertiary Structures
TITLE OF INVENTION: Polypeptide Tertiary Structures
CURRENT APPLICATION NUMBER: US/09/788,006
CURRENT PILING DATE: 2001-02-16
SOFTWARE: Patentin version 3.0
SSEQID NO 107
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                    56.2%; Score 18; DB 15; Length 7; 57.1%; Pred. No. 1e+06; 2; Indels Live 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-107
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US-09-788-006-108
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75.0%;
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             Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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FTIDSSS 7
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US-10-154-971-29
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Gaps

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APPLICANT: DATABLE, CONTINUATION TO APPLICANT: APPLICANT: DATABLE, CONTINUATION APPLICANT: Benard, Claire
APPLICANT: Rebit ' Handa
APPLICANT: Rebit ' Handa
APPLICANT: ACAIT, ' Handa
APPLICANT: Lakowski ' Bernard
ITILE OF INVENTION: CIK-2 WUCLERIC ACIDS, POLYPEPTIDES, AND USES THEREOF
ITILE OF INVENTION: CIK-2 WUCLERIC ACIDS, POLYPEPTIDES, AND USES THEREOF
ITILE OF INVENTION CIK-2 WUCLERIC ACIDS, POLYPEPTIDES, AND USES THEREOF
ITILE REFERENCE: 11202-06-999
CURRENT FILING DATE: 2003-01-22
PRIOR PLILING DATE: 2001-06-20
PRIOR PLILING DATE: 2001-06-20
PRIOR PLILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/254,932
PRIOR PLILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3:2
SEQ ID NO 11
                    Score 18; DB 14; Length 7; Pred. No. 1e+06; 1; Mismatches 2; Indels
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56.2%; Score 18; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 18+06;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10349507
Publication No. US20030199002A1
GENERAL INFORMATION:
APPLICANT: Hekimi, Siegfried
Query Match
Best Local Similarity 57.1%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                         1 FTLTISS 7
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US-10-006-869-637
US-10-006-869-637
Sequence 637, Application US/10006869
Publication No. US2030082166A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Branch Sequence Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAPHERIN' MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C7
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 637
LENGTH: 7
                                                                                            JULIAND TO SEQUENCE 11, APPLICATION US/10267565

PUBLICANT: Gately, Maurice
APPLICANT: Gately, Maurice
APPLICANT: Gately, Maurice
APPLICANT: Gabler, Ulrich
APPLICANT: Gabler, Ulrich
APPLICANT: Humes, Jeffery
APPLICANT: Podiaski, Frank
APPLICANT: Humes, Jeffery
APPLICANT: Stern, Alvin
TITLE OF INVENTION: LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
TITLE OF INVENTION: LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
TITLE OF INVENTION: LYMPHOCYTE NS. 10570-01-23
FRIOR APPLICATION NUMBER: 09/401,839
FRIOR PELING DATE: 1999-09-22
FRIOR APPLICATION NUMBER: 09/459,151
FRIOR APPLICATION NUMBER: 07/857,023
FRIOR APPLICATION NUMBER: 07/857,023
FRIOR APPLICATION NUMBER: 07/857,023
FRIOR APPLICATION NUMBER: 07/857,038
FRIOR APPLICATION NUMBER: 07/857,038
FRIOR APPLICATION NUMBER: 07/857,038
FRIOR APPLICATION NUMBER: 07/857,038
FRIOR APPLICATION NUMBER: 07/85,708
FRIOR FILING DATE: 1999-06-09
FRIOR FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 43
SOFTWARE FASERER FASERE FOR WINDOWS VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.2%; Score 18; DB 12; Length 7; 100.0%; Pred. No. 1e+06;
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
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ORGANISM: Homo sapiens
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US-10-395-032-637

US-10-395-032-637

Sequence 637, Application US/10395032

Publication No. US20030229199A1

GENERAL INFORMATION

APPLICAMY: Blaschuk, Orest W.

APPLICAMY: Symonds, James Matthew

APPLICAMY: Symonds, James Matthew

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR WODULATING NONCLASSICAL

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

FILLS REFERENCE: 100086.407C9

CURRENT APPLICATION NUMBER: US/10/395,032

CURRENT FILING DATE: 2003-03-21

NUMBER OF SEQ ID NOS: 4052

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 637

LENGTH: 7

LENGTH: 7

LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative linear modulating agent based on
OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
CHER INFORMATION: recognition sequence
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June 1, 2004, 11:18:42; Search time 34.6667 Seconds (without alignments) 56.387 Million cell updates/sec
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(ggn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
(ggn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
(ggn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
(ggn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
(ggn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                           OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

tion	Sequence 18, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 107, App Sequence 107, Appl Sequence 17, Appl Sequence 18, Appl
Description	Sequence 11 Sequence 61 Sequence 63 Sequence 63 Sequence 17
SUMMARIES	US-10-150-654A-18 US-10-267-565-11 US-10-006-669-637 US-10-395-032-637 US-09-788-006-107 US-09-777-91A-17 US-09-777-921A-17 US-09-777-921A-17 US-09-777-921A-17 US-10-698-489-14 US-10-156-820-59 US-10-156-97 US-10-159-006-47
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Sequence 46, Appl	equence 69, 7	16	E e	φ	'n	Ä	m	4,	9	Sequence 394, App	ო	,	39	Sequence 650, App	Ψ	9	402	402	Sequence 402, App	650	243	55,	47,	5, 1	124	7, App	12,	B, App	Sequence 7, Appli
US-10-054-712-46	-832-723-6	96-288	19-986-6	0-303-33	0-022-06	US-10-461-863-164	-10-286-18	6	0-315-96	0-317-251A-	0-317-252A-3	9-876-38	-10-105-930-3	٣	0-287-892-	0-288-3	0-315	0-317-2	-31	0-395-(	0-394-5	0-418-9	3-10-374-4	US-09-056-160B-5	-09-056-16	9-87	-09-734-41	9-0	US-09-947-137-7
16	σ	σ	70	14	14	12	14	14	14	14	14	σ	14	14	14	14	14	14	14	15	15	16	16	σ	σ	6	6	σ	6
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16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36			39		41	42	43	44	45

## ALIGNMENTS

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Search completed: June 1, 2004, 11:16:14 Job time : 49.6667 secs

c amino acid residues of the first segment, together with an additional amino acid residues of the first segment, together with an additional between a mino acid residue(s) adjacent to the first amino acid sequence. The between and disuphide bridges of a polypeptide are determined by identifying a superstructure encompassing alternative beta-strand arrangements, representing the superstructure by an integer-linear of programming mathematical model, with the model maximising the total hydrophobic contact energy, and then solving the model. The method can also apply energy modelling with a full atom force field potential to generate a constrained global optimisation problem, optionally applying a corsination problem to determine the three-dimensional structure of polypeptide and is accurate and reliable. The sequences presented in ABU12184-ABU12235 are the pentapeptides of the Streptomyces griseus immungolobulin-binding domain from streptococcal protein G, 1081, which were used to predict the alpha-helical regions in an example of the method of the invention

Sequence 5 AA;

Query Match 53.1%; Score 17; DB 6; Length 5; Best Local Similarity 75.0%; Pred. No. 1.40+06; Matches 3; Conservative 1; Mismatches 0; Indels 0; Indels

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Gaps .; 0

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cc inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal.

Cc mammal, inhibiting metastass of a cancer in a mammal, inhibiting cancer in a mammal, inhibiting metastass of a cancer in a mammal, inhibiting cancer in a mammal, inhibiting metastass of a cancer in a mammal, inhibiting stimulating completes in a nonclassical cadherincer completes in a mammal, inhibiting stimulating contral nervous system, treating ademyelinating neurological disease, contral nervous system, treating a demyelinating neurological disease, concreasing vasopermeability in a mammal, enhancing deficient of formal cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for conclassion of foreign tissue, or enhancing adhesion of foreign tissue in a conclassion and a despectation and diagnosis and in bioreactors. AAY60592 to AAX64572 represent specifically claimed peptides, and conclassions the conclusions and AAX66531 to AAX64572 represent specifically claimed peptides, and conclusions the conclusions and AAX66531 to AAX64572 represent specifically claimed peptides, and conclusions and AAX66531 to AAX64572 represent specifically claimed peptides, and conclusions and AAX6653 to Concern the conclusions and AAX66653 to Concern the conclusions in the conclusions and AAX6653 to Concern the concerns the concerns
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Local Similarity Query Match

Score 18; DB 3; I Pred. No. 1.4e+06; 1; Mismatches 2; 56.2%; 4; Conservative 1 FILTISS 7 1 FTIDSSS 7 Best Loca Matches 8 g

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2; Indels Length 7;

ABB84102 standard; protein; 7 AA. 09-SEP-2002 ABB84102; RESULT 14
ABB84102
AZC ABB84
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AZC ABB84
XX
DT 09-SE
DE Human
XX
CS HOMO
CS CC This
CC STRUCT
COLL
XX
CC This
CC STRUCT
CC ST

(first entry)

Human single chain diabody CEAGal fragment #2.

Antibody; multimer; cytostatic; detection; immunoassay; tumour.

Homo sapiens,

/note= "Unidentified residue" Location/Qualifiers Key Misc-difference

DE10060140-A1

06-JUN-2002.

04-DEC-2000; 2000DE-01060140

(VECT-) VECTRON THERAPEUTICS IMT AG. 04-DEC-2000; 2000DE-01060140

Kontermann R;

WPI; 2002-520984/56.

New multimer of single-chain antibodies, useful e.g. for diagnosis drug delivery, has four variable chains linked through peptides of controlled length.

Example 1; Fig 2B; 16pp; German.

This invention describes a novel multimer containing at least two attibodies, each, independently, comprising a polypeptide chain of structure V1-PA-V2-PW-V3-PB-V4 where V1-V4 = variable domains; PA, PB and PM = peptide linkers with PA and PB containing 0 or 1 amino acid. The

The invention discloses a ASTRO-FOLD approach for the ab anitio prediction method for determining the existence and location of alphabeliax regions and arrangement of beta-sheets and disulphide bridges of a polypeptide. The method comprises defining the first segment of the amino acid sequence, performing atomistic modelling upon each segment of senerating an ensemble of low energy conformations, determining the entropic and free energy for each segment and then ascertaining the equilibrium probabilities for helical clusters. The segments consist of pentapeptides, with each further segment including a majority of the

Example 1; Page 59; 147pp; English.

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products of the invention have cytostatic activity. The multimers described can be used for diagnostic detection, in essentially standard immunoasay methods, and for binding at least one component and/or fused protein or peptide to a cell, especially to deliver a toxin or for infection, transformation or transfection of the cell. (I), or nucleic acid (II) encoding it, or vectors containing (II), are useful for treating tumours. The multimers are relatively small (about 110 Kpa formers) but have multiple binding sites to ensure high binding affinity. This sequence represents a fragment of the single chain diabody CBAGal (composed of a tumour marker carcinoembryonic antigen fragment and E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcal protein G, 1GB1, alpha helix prediction pentapeptide #51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASTRO-FOLD; ab anitio; alpha-helix; beta-sheet; disulphide bridge; atomistic modelling; low energy conformation; entropic energy; free energy; equilibrium probability; helical cluster; integer-linear; mathematical model; hydrophobic contact energy; actom force field potential; global optimisation; toreion angle; dynamic algorithm; three-dimensional structure; tertiary structure; immunoglobulin-binding domain; protein G; 1681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determining helix regions, and beta sheets of polypeptide, involves partitioning peptide, atomistic modeling by selected force, generating ensemble low energy, and calculating free energies for each peptide.
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                           Score 18; DB 5; Length 7; Pred. No. 1.4e+06; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   ABU12234 standard; peptide; 5 AA.
                                                                                                                                                                                                                                           56.2%;
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les 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces griseus.
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                                                                                                                                                                                                             Sequence 7 AA;
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                                                                                                                                                                                                                                         Query Match
Best Local Si
Matches
                                                                                                                                                                              invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU12234;
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
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ID ABU1
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ABRS5412-20 represent conserved region of a phospholipase C (PLC)-zeta polypeptide. PLC-zeta polypeptides are capable of triggering calcium oscillations in occytes. The PLC-zeta isoform is expressed specifically in mammalian sperm, and is an addispection for mammalian fertilisation and embryo development. PLC-zeta polymucleotides are useful for preparing a composition for diagnosing or treating infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated antibody has been developed which binds specifically to cytotoxic lymphocyte maturation factor (CLMF) and neutralises CLMF induced proliferation by more than 50% in a CLMF dependent T cell growth assay and/or inhibits binding of at least 60% of the factor to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytotoxic lymphocyte maturation factor; CLMF; cytokine; synergize; interleukin 2; IL-2; human; lymphoblastoid cell; detection; purifying; proliferation; cytotoxic T cell; transplantation; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies to cytotoxic lymphocyte maturation factor - useful for detecting, purifying, and/or blocking proliferation and activation of cytotoxic T cells, such as in transplantation(s).
                                                                                                                                               New phospholipase C-zeta gene, useful for preparing a composition for diagnosing or treating infertility.
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100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tryptic 40 kD subunit CLMF peptide off PVDF #4.
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                                                                                                                                                                                                                                            Claim 10; Page 68; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW58711 standard; peptide; 7 AA.
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90US-00520935.
90US-00572284.
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Gubler UA;
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Best Local Similarity 100.
Matches 4; Conservative
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                       Lai T;
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phytohaemagglutinin (PHA) activated peripheral blood lymphocyte (PBL) blasts as determined in a CLMF receptor binding assay. CLMF is a heterodimeric protein having a molecular weight band of 75 kD, determined by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) under non-reducing and/or reducing conditions, providing a first subunit having a molecular weight band of 40 kD and a second subunit having a molecular weight band of 40 kD and a second subunit having a molecular weight of 35 kD. The present sequence represents a tryptic 40 kD cLMF peptide off polyvingleen difluoride (PVDF), from an example of the present invention. The antibody can be used for the purification and/or detection of CLMF. It is also used in therapeutic treatments which require selective blocking of proliferation and activation of cytocoxic T cells (CTLs) such as in transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; bleadherin; cadherin-5; cadherin-7; cadherin-13; cadherin-13; cadherin-15; T-cadherin; pB-cadherin; protocadherin-12; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmocallin; cancolum binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g.
                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cadherin-related neuronal receptor CAR sequence SEQ ID NO:637.
                                                                                                                                                                                                                                                                                Length 7;
                                                                                                                                                                                                                                                                                Score 18; DB 2; L
Pred. No. 1.4e+06;
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                                                                                                                                                                                                                                                                              56.2%; Scoi
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY64225 standard; peptide; 7 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-00073040.
98US-00187859.
99US-00234395.
99US-00264516.
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                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-038791/03.
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                      2 TLTI 5
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                                                                                                                                                                                                                                            Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-1998;
20-JAN-1999;
08-MAR-1999;
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An injury healing and postsurgical tissue recovering integrin activating peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phospholipase C zeta; PLC-zeta; calcium oscillation; oocyte; sperm; embryo; infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid seguence of a conserved region of PLC-zeta protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.4%; Score 19; DB 4; Length 6; 60.0%; Pred. No. 1.46+06; ive 2; Mismatches 0; Indels
                                                                                                                                                                                       Integrin stimulant; vulnerary; injury healing; postsurgical tissue recovery.
                                                                                                                                                   Integrin activating peptide SEQ ID NO 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR55418 standard; peptide; 5 AA.
                                       AAM51422 standard; peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 3; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                               (HISM ) HISAMITSU PHARM CO LID.
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28-JUN-2002; 2002GB-00014945.
                                                                                                                                                                                                                                                                                                                                                        31-JAN-2000; 2000JP-00022469.
                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-2000; 2000JP-00022469.
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Best Local Similarity 60.v.
3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6 AA;
                                                                                                                                                                                                                                              Unidentified.
                                                                                                                08-JAN-2002
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                                                                            AAM51422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR55418;
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ABR55418
     RESULT 10
                         AAM51422
                                                           g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to diagnosing the presence of colon cancer, metastases of colon cancer, staging colon cancer, monitoring colon cancer for the onset of metastasis or monitoring a change in stage of colon cancer in a patient. The method involves determining a colon specific gene (CSG) in cells, tissues or bodily fluids and comparing it with levels of CSG in cells, tissues or bodily fluids from a normal human control. Colon cancer can be treated by administering a molecule which down regulates the expression or activity of CSG. An immune response against a target cell expressing CSG can be induced by delivering an immune response is mounted. Therapeutic agents are useful for imaging colon cancer in a patient by administering an agent labelled with paramagnetic ions or a radioisotope to the patient. They are also useful for paramagnetic ions or a radioisotope to the patient. They are also useful for the disease. Sequences ANUSESCA PANUSSCO represent human colon specific protein antibody binding sites used in the method of the
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                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing, staging or monitoring colon cancer involves determining a colon specific gene in cells, tissues or body fluids in patient, and comparing it with levels of the gene from a normal human control.
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                                                                                                                                                                                                                                                                                                                 Human colon specific polypeptide antibody binding site #31.
 Score 21, DB 3; Length 7; Pred. No. 1.4e+06; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 100.0%; Pred. No. 1.4e+06; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    Human; colon specific gene; CSG; cytostatic; metastasis; colon cancer staging; antibody binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 21; 52pp; English.
                                                                                                                                                                                                    AAU85454 standard; peptide; 5 AA.
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Ouery Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity
Matches 4; Conserv
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                                                                          1 FTLTIS 6
                                                                                              SETIS 7
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2 FTLT 5
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                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                          AAU85454;
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AAU8546

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The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40677) which forms part of a scaffold protein. S4 is a bet strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at the teast 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands
                                                                                                                                                                                                                        Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New scaffold protein, useful for stabilizing antigens used as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S4 derivative #9, beta strand of scaffold protein structure.
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Pred. No. 1.4e+06;
.; Mismatches 0; Indels
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                                                                                          Hoogenboom H,
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                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 15; 68pp; English
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83.3%;
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                               (INNO-) INNOGENETICS NV.
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                                                                                              Desmet J, Hufton S,
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Best Local Similarity
5; Conserv?
                                                                                                                                                             WPI; 2000-665002/64.
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form two beta sheets $1/$4/$3 and $6/$5/$2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands Al-A3 are included in the structure the caffold is constructed of two beta sheets, with the structures the caffold is constructed of two beta sheets, with the structures of Al/$1/$4/$3 and $6/$5/$2/$2/$A2/$3. The beta strands are connected to each other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules for example, one surface of the scaffold may be bound to a protein which binds to a tumour antigen. This will carried the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target the complex to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
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Pred. No. 1.4e+06;
; Mismatches 0; Indels
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Best Local Similarity 66.7
Matches 4; Conservative
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Gaps ö Sequence 7 AA;

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Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY4067) which forms part of a scaffold protein. S4 is a beta estrand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least beta-strands. The scaffold protein his constructed of beta crands all s6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands of functionally equivalent derivative of these sequences. The beta strands of the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures of the next by hydrogen bonds, which pease trands are connected to the rate of incomplex of two beta sheets, with the structures of two ther via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens or whole proteins such as receptors, or their fragments. It may be used to the complex to tumour cells. Protein may be used to carget the complex to tumour cells. Another surface may be bound to a protein such as receptors, or their may also be used to tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines
                                                                                                                                                                                                                   New scaffold protein, useful for stabilizing antigens used as vaccines
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                                                                                                                               Sablon
                                                                                                                                 Desmet J, Hufton S, Hoogenboom H,
                                                                                                                                                                                                                                                                   Disclosure; Page 6; 105pp; English.
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FTLSIS 7
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                                           31-MAR-1998;
31-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
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SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
diabetic retinopathy; atherosclerosis.
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                                                                                                                                                  Scaffold protein SCA S4 peptide SEQ ID NO: 136.
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                   AAB30075 standard; peptide; 7 AA
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Best Local Similarity 83.3.,

Best Local Similarity 63.3.
                                                                                                       (first entry)
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RESULT 5
AAY40736
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Gaps

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Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine; tumour; chemotherapeutic agent.

S4 derivative #11, beta strand of scaffold protein structure.

(first entry)

01-DEC-1999

AAY40737;

AAY40737 standard; peptide; 7 AA.

AAY40737 RESULT

FTLTIS

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or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold may be bound to a protein which binds to a tumour antigen. This will target the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines
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87.5%; Score 28; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels
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Desmet J, Hufton S, Hoogenboom H, Sablon E;

VPI; 1999-542958/46.

98EP-00870065.

31-MAR-1998; 31-MAR-1998;

EP947582-A1. 06-OCT-1999

Synthetic.

(INNO-) INNOGENETICS NV.

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Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta servand peptide which forms part of a beta sheer. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 6 beta-strands. The scaffold protein which contains at least 6 beta-strands. The scaffold protein is constructed of beta strands. The scaffold protein is constructed of beta strands also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands of forms two beta sheets $1/84/83 and $6/85/$2 vith each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures of the next by hydrogen bonds, which be beta strands are connected to other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface may be bound to a protein which binds to a tumour antigen. The scaffold protein may be used to target tumour cells. Therefore the scaffold protein may be used to target tumour cells. Therefore the scaffold protein may be used to target tumour cells. Therefore the scaffold protein may be used to stabilize individual peptides in a peptide library and may be used in stabilize antigens used as vaccines
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2 YTLTIS 7
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Matches
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RESULT 4

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87.5%; Score 28; DB 3; Length 7; 100.0%; Pred. No. 1.4e+06; tive 0; Mismatches 0; Indels

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	GenCore version 5.1.6	27	16
	Copyright (c) 1993 - 2004 Compugen Ltd.	28	16
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OM protein - pr	OM protein - protein search, using sw model	31	16
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	(without alignments)	34	16
	43.310 Million cell updates/sec	35	16
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Scoring table:		41	16
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Searched:	1586107 segs, 282547505 residues	44	16

A Geneseq 29Jan04:\*

1: geneseqp1980s:\*

2: geneseqp2001s:\*

3: geneseqp2001s:\*

5: geneseqp2003s:\*

6: geneseqp2003bs:\*

7: geneseqp2003bs:\*

8: geneseqp2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES	
Result		* Ouery				
No.	Score	Match	Match Length DB	DB DB	ID	Description
п	28	87.5	7	7	AAY40738	
<b>C</b> 1	28	7	7	m	AAB30076	6 Sca
m	25	78.1	7	7	AAY40737	
4,	25	78.1	7	ო	AAB30075	'n
S	24	75.0	7	~	AAY40736	Aay40736 S4 deriva
v	24	75.0	7	m	AAB30074	Aab30074 Scaffold
7	21	65.6	7	~	AAY40735	Aay40735 S4 deriva
80	21	65.6	7	m	AAB30073	Aab30073 Scaffold
6	20	62.5	ഗ	'n	AAU85454	
10	19	59.4	9	4	AAM51422	422
11	18	56.2	S	φ	ABR55418	
12	18	56.2	7	N	AAW58711	Н
13	18	56.2	7	ጣ	AAY64225	Aay64225 Cadherin-
14	. 1 <b>8</b>	56.2	7	w	ABB64102	Abb84102 Human sin
15	17	53.1	2	9	ABU12234	
16	17	53.1	Ŋ	9	ABU12235	'n
17	17	53.1	φ	N	AAW39453	Aaw39453 Human T c
18	17	53.1	φ	7	AAW75358	Aaw75358 Hexapepti
19	17	53.1	φ	N	AAW75290	Aaw75290 Hexapepti
20	17	53.1	φ	φ	AAE31832	Aae31832 Androgen
21	17	53.1	7	N	AAR07656	Aar07656 Ribonucle
22	17	53.1	7	c۷	AAY40723	_
23		53.1	7	m	AAB30062	2 80
24	17	53.1	7	4	0	Aam44200 H11 bindi
25	17	53.1	7	4	AAM44205	H11

Aap93345 Portion o	Aar93089 GAL4 DNA	Aaw61443 Gal 4 pro	Aaw76753 Murine si	Aaw92487 Murine Ga	Aay90491 GAL4 DNA	Aab03571 Nuclear c	Aab36961 Peptide #	Aab60836 Peptide #	Abj11455 Human 125	Aae28111 Human imm	Abu72693 Novel pro	Abr45358 Staphyloc	Abr46478 Staphyloc	Abr44966 Staphyloc		Abr46870 Staphyloc		Abj57003 184P1E2-r	Aar72775 Mammalian
1 AAP93345	2 AAR93089	2 AAW61443	2 AAW76753	2 AAW92487	3 AAY90491	3 AAB03571	4 AAB36961	4 AAB60836	5 ABJ11455	5 AAE28111		6 ABR45358	6 ABR46478	6 ABR44966	6 ABR45694	6 ABR46870	6 ABR46086	6 ABJ57003	2 AAR72775
Φ	φ	φ	φ	9	9	Q	9	φ	9	9	9	9	9	9	9	9	9	9	7
50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0		50.0		50.0
16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16
26		28		30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

RESULT 1

92273

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

AAY40738;  01-DEC-1999 (first entry) S4 derivative #12, beta sts tumour; chemotherapeutic synthetic. EP947582-A1. 06-OCT-1999. 31-MAR-1998; 98EP-00870C 31-MAR-1998; 98EP-00870C 31-MAR-1998; 98EP-00870C WPP: 1999-542958/46. New scaffold protein, usef	AAY4	AAY40738 TD AAY40730 Standard Loutid	, , , , , , , , , , , , , , , , , , ,
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	∃ 8	Hurton S,	Sablon
	œ >	WPI; 1999-542958/46.	
• •	<b>∮</b> [+ ]	New scaffold protein, use	ful for stabilizing antigens used as vaccine
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Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-V40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands of converted to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure of the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure of scaffold is constructed of two beta sheets, with the structure of the roll of the amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens Disclosure; Page 6; 105pp; English. 

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4 TISS 7
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P83492;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Alkaline protease Gr3 (EC 3.4.21.-) (Fragment)
Bionectria cohroleuca (Gliocladium roseum).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.
                                                                                                                                                                                                                                                                                               Query Match 21.9%; Score 7; DB 3; Length 7; Best Local Similarity 50.0%; Pred. No. 1e+06; Matches 2; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                    SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION STRAIN-Gr87;
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TQSN 5
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STRAIN-Cooper,
MEDLINE-95113343; PubMed=7793062;
MEDLINE-95113343; PubMed=7793062;
Luck C., Benes V., Lu Z., Kutish G.F., Paces V., Rock D.,
Lucchworth G.J., Schwyzer M.;
"Nucleotide sequence analysis of a 30-kb region of the bovine
herpesvirus 1 genome which exhibits a collinear gene arrangement with
the UL21 to UL4 genes of herpes simplex virus.";
Virology 210:100-108(1995).
BMBL; Z48053; CAA88130.1; -.
Hypotherical protein.
NON TER 1
SEQÜENCE 7 AA; 758 MW; 6DD33455BIF1BICO CRC64;

Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus. NCBI\_TaxID=10320;

SEQUENCE FROM N.A.

Bovine herpesvirus 1.

01-NOV-1996 (TrEMBLrel. 01, Created)
1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical procein (Pragment)

PRT;

PRELIMINARY;

Q65578 Q65578;

RESULT 15 Q65578 21.9%; Score 7; DB 12; Length 7;

Query Match

Search completed: June 1, 2004, 11:18:36 Job time: 33.3333 secs

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6 AA; 675 MW; 6321B415B05DB000 CRC64;
                                                                Query Match

Quest Local Similarity 100.00

Best Local 2; Conservative
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Aad Al protein (Fragment).
AAD Al.
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P72081;
01-FEB-1997 (
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01-NOV-1996
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P72081
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                                                                                                                                                                                                                                                                                                                       MEDINE-ZORANGO, TISSUE-Leaf;
MEDINE-ZORANGO, TISSUE-Leaf;
MEDINE-ZORANGO, TISSUE-Leaf;
MEDINE-ZORANGO, MEDINE-
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01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 50S ribosomal protein L10 beta (Fragment).
Spinacia oleracea (Spinach)
Bukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Spinacia.
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01-UTN-2000 (TrEMBLrel. 14, Created)
01-UTN-2000 (TrEMBLrel. 14, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 50S ribosomal protein L10 gamma (Fragment).
Expinacia oleracea (Spinach).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Spinacia.
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PROSITE; P801109; RIBOSOMAL L10; PARTIAL.
Ribosomal protein; Chloroplast; rRNA-binding.
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SEQUENCE
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P82182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of the cmcH genes of Nocardia lactamdurans and Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem O-carbamoyltransferase for cephamycin biosynthesis.";
Gene 162:21-27(1999)
EMBL; 221682; CAA79797.1;
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MEDLINE=94079349; PubMed=8257126;
Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;
"Analysis of the agc(3)-VIa gene encoding a novel 3-N-
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=96009872; PubMed=7557411;
Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
Liras P.;
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Enterobacteriaceae; Enterobacter.
NCBI_TaxID=550;
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     Length 6;
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                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
3'-methylcephem hydroxylase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 08, Last annotation update)
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EMBL; M88012; AAA16193.1; -.
25.0%; Score 8; DB 10;
100.0%; Pred. No. 1e+06;
iive 0; Mismatches 0
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RESULT 6

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P82445 PRELIMINARY; PRT; 7 AA.
P82445.
01-070-2000 (TrEMBLrel. 14, Created)
01-070-2000 (TrEMBLrel. 14, Last sequence update)
01-070-2003 (TrEMBLrel. 24, Last annotation update)
01-070-2003 (TrEMBLrel. 24, Last annotation update)
10 kna cell awall protein (Fragment).
Nicotiana tabacum (Common tobacco).
Sukaryota, Viidigplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
1amiids; Solanales; Solanaceae; Nicotiana.
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MEDLINE-22056123; PubMed=12060770;
Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
Berenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
Beframn D., Korn K., Selbig J.;
"Diversity and complexity of HIV-1 drug resistance: A bioinformatics approach to predicting phenotype from genotype.";
Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
EMBL; AP347267; AAX32344.1; -.
NON TER
1 1
SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
STRAIN=CV. PETIT HAVANA;
Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
Woltaszek P., Bolwell G.P.;
"Proteomic study of secondary cell wall proteins from transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.1%; Score 9; DB 10; Length 7; 33.3%; Pred. No. 1e+06; ive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell wall.
NON TER 7 7 8 SEQUENCE 7 AA; 758 MW; 69D2C1E862D1B2A0 CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 planta 0:0-0(2000).
--- SUBCELLULAR LOCATION: CELL WALL.
--- TISSUB SPECIFICITY: XYLEM.
GO; GO:0005618; C:cell wall; IEA.
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Best Local Similarity 33.3
Matches 1; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tobacco culture
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P82181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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PubMed=12112860;
Drews O., Weise W., Reil G., Parlar H., Wait R., Goerg A.;
Dressoure effects step-wise altered protein expression in lactobacillus sanfranciscensis.";
Proteomics 2.765-774(2002).
-!- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN PROTEIN IS: 15 KDA.
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 19, Last sequence update)
Nifk (Pragment).
Nifk (Pragment).
Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothece PCC 8801).
Bacteria, Cyanobacteria; Chrococcales; Cyanothece.
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P83533;
01-JUN-2003 (TEEMBLrel. 24, Created)
01-JUN-2003 (TEEMBLrel. 24, Last sequence update)
01-JUN-2003 (TEEMBLrel. 24, Last annotation update)
Unknown protein from 2D-page (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Laccobacillus.
NGI_TAXID=1625;
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Microbiology 145:743-753(1999).
EMBL; AF003700; AAC35193.1; -.
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MEDLINE-2-3-11;
MEDLINE-20011291; PubMed=10542330;
Pobhling S., Piepersberg W., Wehmeier U.F.;
Pobhling S., Piepersberg W., Wehmeier U.F.;
Manalysis and regulation of the sec Y gene from Streptomyces griseus
N2-3-11 and interaction of the SecY protein with the SecA protein.";
Biochim. Biophys. Acta 1447:298-302(1999).
EMBL; X95915; CAA65160.1; -.
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PubMed=12112866;
Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
Drews O., weiss W., Reil G., Parlar H., Wait R., Goerg A.;
High pressure effects step-wise altered protein expression in
Lactobacillus sanfranciscensis.";
Proteomics 2.765-774(2002).
-!- MISCELLANDUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
PROTEIN IS: 15 KDA.
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01-UTM-2003 (TrEMBLrel. 24, Last sequence update)
01-UTM-2003 (TrEMBLrel. 24, Last sequence update)
UNANDWA TOTEMBLER 1. 24, Last annotation update)
UNANDWA PROTEIN From 2D-page (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
NCBI_TaxID=1625;
                                                                                                                                                                                                                                                                                                                 Streptomyces griseus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1911;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RplO protein (Fragment).
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                                                                                                                                                                                                                                                                Kim Y.-C.;
Submittes (FBB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U88298; AAB66311.1; -.
GO; GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
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Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    37.5%; Score 12; DB 2; Length 7; 20.0%; Pred. No. 1e+06; artive 4; Mismatches 0; Indels
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STRAIN=Bristol N2;
Bradshaw H., Graws T., Blair T.;
"The sequence of C. elegans cosmid W01B11.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson R.;
Submitted (JUN 2003) to the EMBL/GenBank/DDBJ databases.
EMBL; A7043704; AA038592.1;
Hypothetical protein.
SEQUENCE 7 AA; 874 MW; 72D1A9DB5041A6F0 CRC64;
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Q721C0;
01-0CT-2003 (TrEWBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein W01B11.6.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 7 AA; 868 MW; 71A452D1A699D460 CRC64;
                                                                   Catechol-2,3-dioxygenase (Fragment)
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MEDLINE=99069613; PubMed=9851916;
                                                                                                             Sphingomonas chungbukensis.
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                                                                                PRELIMINARY;
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                                                                                                                              June 1, 2004, 10:53:46; Search time 31.3333 Seconds (without alignments) 70.488 Million cell updates/sec
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
-! SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Amidation.
MAIDATION.
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Eur. J. Biochem. 250:727-734(1997).
-!-FUNCTION: May act as a neurotransmitter or neuromodulator.
-!-SIMILARITY: Belongs to the allatostatin family.
Mouropeptide; Amidation; Multigene family.
MOD RES
7 AMIDATION.
SEQÜENCE 7 AA; 781 MW; 672879CDCB476420 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                               Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleccyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                 1; Indels
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       Length 7;
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7 AA; 873 MW; 672879CABB569350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Cerebral ganglion, and Thoracic ganglion; MEDLINE=98121193; PubMed=9461295;
                         Pred. No. 1.4e+05;
0; Mismatches 1
    Score 8; DB 1;
Pred. No. 1.4e+0!
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Carcinustatin 5.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Cydiastatin 7.
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MEDLINE=98054539; Pubmed=9392829;
25.0%;
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Best Local Similarity 66.7:
....hes 2; Conservative
Query Match
Best Local Similarity 66.7
Matches 2; Conservative
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25.0%; Score 8; DB 1; Length 7;

Query Match

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Pred. No. 1.4e+05;
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Best Local Similarity 66.7%;
Matches 2; Conservative
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Search completed: June 1, 2004, 11:16:49 Job time : 9.66667 secs

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Local Similarity
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P81806;
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Query Match
Best Local S
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ALL3_CARMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                "Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, primary structure and synthesis.", Regul. 27:49-57(1992).
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                                                                                                                                                                                                                         Locusta migratoria (Migratory locust).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Corpora cardiaca;
MEDLINE=92262851; PubMed=1585017;
Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
de Loof A.;
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Carcinus maena 8.
Carcinus maena 9.
Carcinus maena 8.
Carcinus 8.
Carcinus 8.
Carcinus 9.
CEI TaxID=6759;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                              6 AA.
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PIR; A61068; A61068.
Neuropeptide; Amidation.
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Best Local Similarity
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Incorpe A.;
Insolation and identification of multiple neuropeptides of the "Isolation and identification the shore crab Carcinus maenas.";
Bur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SIMILMAITY: Belongs to the allatostatin family.
SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUBECerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryott, Metazoa, Arthropoda, Crustacea, Malacostraca,
Eumalacostraca, Eucarida, Decapoda, Pleccyemata, Brachyura,
Eubrachyura, Portunoidea, Portunidae, Carcinus.
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  Length 7;
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Score 8; DB 1; Le
Pred. No. 1.4e+05;
); Mismatches 1;
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30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots, asterids,
campanulids, Apiales, Apiaceae, Apioideae, Scandiceae, Daucinae,
                       Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
Citrobacter freundil and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
-!- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
-!- PATHWAY: Biotin blosynthesis; last step.
-!- SIMILMARITY: Belongs to the biotin and lipoic acid synthetases family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSK_DAUCA STANDARD; PRT; 5 AA.
PS98561;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         embryos.
-!- SUBCELLULAR LOCATION: Secreted.
-!- FUM: SULfation is important for activity and for the binding to
    putative membrane receptor (By similarity).
-!- SIMILARITY: Belongs to the phytosulfokine family.
Growth factor; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CV. US-Harumakigosun,
MEDLINE=20212743; PubMed=10750705;
Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
Kamada H., Sakagami Y.,
"A secreted peptide growth factor, phytosulfokine, acting as a
stimulatory factor of carrot somatic embryo formation.";
Plant Cell Physiol. 41:27-32 (2000).
-i- FUNCTION: In presence of 2,4-D, stimulates proliferation of the
cells, but does not stimulate differentiation into the somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.0%; Score 8; DB 1; Length 5; 100.0%; Pred. No. 1.4e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.0%; Score 8; DB 1; Length 5; 50.0%; Pred. No. 1.4e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 3 SULPATION.
5 AA; 687 MW; 76CIBBS04B300000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHYTOSULFOKINE-BETA.
SULFATION.
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M21922; -; NOT_ANNOTATED_CDS.
PIR, 140698; 140698.
Biotin biosynthesis; Iron-sulfur; Transferase.
NON TER.
5
      MEDLINE=89006280; PubMed=2971595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.07
Local 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Daucus carota (Carrot)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4039;
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MOD_RES
MOD_RES
SEQUENCE
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"Isolation and structure of the Streptococcus faecalis sex pheromone, CAM373.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Citrobacter freundii.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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Eur. J. Biochem. 250:7734(1997).
-!-FUNCTION: May act as a neurotransmitter or neuromodulator.
-!-SIMILARITY: Belongs to the allatostatin family.
Nouropeptide; Amidation; Multigene family.
MOD RES
- S
- AMIDATION (POTENTIAL).
SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;
                                                                                                 -1- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR SPECIFICITY OF PHEROMONES TO PLASHIDS.
-1- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
PIR; A25269; A25269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUBECETED and lion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                         FEBS Lett. 206:69-72(1986).
-!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
HARBORING PAM373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
1-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carcinus maenas (Common shore crab) (Green crab).

Bukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,

Bumalacostraca, Eucarida, Decapoda, Pleocyemata, Brachyura,

Bubrachyura, Portunoidea, Portunidae, Carcinus.
                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                                                  Length 7;
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                                                                                                                                                                                                                   7 AA; 734 MW; 75BDD72059C05DB0 CRC64;
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                                                                                                                                                                                                                                                             28.1%; Score 9; DB 1; Le 66.7%; Pred. No. 1.4e+05; Live 0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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P81817;
                                                                                                                                                                                              Pheromone.
SEQUENCE
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Sex pheromone cCF10.
Enterococcus faecalis (Streptococcus faecalis).
Bacteria, Firmicutes, Lactobacillales, Enterococcaceae, Enterococcus.
NCBI_TAXID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-PEB-1991 (Rel. 17, Last annotation update)
Sex pheromone cAM373 (Clumping-inducing agent) (CIA).
Bacteria; Fareis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TAXID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89008313; PubMed-3139658; Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M., Adsit J.C., Dunny G.M., Suzuki A.; Suzuki A.; Sizutuki A.; Siz
                                                     TISSUE=Skin secretion;
Wabbitz P.A., Boule J.H., Tyler M.J., Wallace J.C.;
Wappides from the Shue Jands of the Australian buzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEGUENCE.
MEDILDE-87005252; PubMed-3093276;
Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada
White B.A., An F.Y., Clewell D.B., Suzuki A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.2%; Score 10; DB 1; Length 5; 33.3%; Pred. No. 1.4e+05; varive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                   rubella.".

- usust. J. Chem. 52:639-645(1999).

- I SUBELLULAR LOCATION: Secreted.

- I TISSUE SPECIFICITY: Skin.

- I TISSUE SPECIFICITY: Skin.

Mob Ras

SEQUENCE 5 AA, 616 MW, 61F2D1A059A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AA; 790 MW; 72C9D2C731B2C740 CRC64;
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Best Local Similarity 33...
Best Local 1, Conservative
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nes 2; Conservative
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P11932;
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CIA_ENTRA
CIA_ENTRA
ACC PIT 01-0C
DT 01
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Matches
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              HAPPER REPORT OF THE THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPOR
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"The structure of new peptides from the Australin red tree frog 'Litoria rubella'. The skin peptide profile as a probe for the study of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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"Peptides from the skin glands of the Australian buzzing tree frog
Librari electrica. Comparison with the skin peptides from Litoria
rubella.",
Aust. J. Chem. 52:639-645(1999).
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Rubellidin 3.2.
Litoria rubella (Desert tree frog).
Elitoria rubella (Desert bree frog).
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinee; Litoria.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
Pelodryadinae, Litoria.

NCBI_TaxID=104895,
[1]
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--- SUBCELDULAR LOCATION: Secreted.
--- TISSUE SUBCRIFICITY: Expressed by the skin dorsal glands.
--- MASS SPECTROMETRY: NW=655; METHOD=FAB.
--- MASS PRECTROMETRY: NW=655; METHOD=FAB.
--- MADALIDian defense peptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.4%; Score 11; DB 1; Length 5; Best Local Similarity 100.0%; Pred. No. 1.4e+05; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.4%; Score 11; DB 1; Length 5; 100.0%; Pred. No. 1.4e+05; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD RES 5 AMIDATION.
SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESULT 4
E104 LITRU
ID E104 LITRU
STANDARD; PRT; 5 AA.
AC P83100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-CCT-2003 (Rel. 42, Last annotation update)
DE Blectrin 4.
OS Litoria Tubella (Desert tree frog).
OC Bliarycta; Metazoa; Chordata; Craniata; Vertebra;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloido
OC NOBI_TAXID=104895;
RN [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
RE32 LITRU
ID RE32 LITRU
AC P82073;
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litoria rub acheta dome canis famil

P82071 P19991 P54714

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Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
Cowfrorne M.;
Submitted (AUG-1998) to Swiss-Prot.
-!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP
cyclohydrolase I. This inhibition is reversed by L-phenylalanine
-!- SUBMIT: Homodimer (By similarity).
-!- SUBMIT: Homodimer (By similarity).
-!- SUBMIT: MT MT MT
--- This Book MW; 71B5B057273B4700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
GFRP MOUSE STANDARD; PRT; 7 AA.

AC P99025;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-2001 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
GN GCHFR OR GFRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2

RE31_LITRU

AC P82072.

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-0CT-2003 (Rel. 42, Last annotation update)

DE Rubellidin 3.1.

OS Litoria rubella (Desert tree frog).

OC Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, OC Amphibia, Barrachia, Anura, Neobatrachia, Hyloidea, Hylidae;

OC Pelodryadinae, Litoria.

NAMPA PARTA (PARTA (PARTA) (PARTA
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Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao
Tyler M.J., Wallace J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.5%; Score 12; DB 1; Length 7; Best Local Similarity 60.0%; Pred. No. 1.4e+05; Matches 3; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                         UC22_MAIZE
CIP1_MYTED
CIP2_MYTED
EI01_LITRU
FARP_MONEX
FAR1_ASCSU
FAR1_HELTI
FAR1_MACRS
FAR1_PROCL
RE21
SUGA
TPIS
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3 LTISS 7
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TISSUE=Liver;
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P82072 litoria rub
P82073 litoria rub
P82100 litoria rub
P20104 enterococcu
P11932 enterococcu
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P13071
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                                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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RE32_LITEU
RE32_LITEU
CCF1_ENTFA
ALI4_CREWA
BIOB_CITER
BIOB_CITER
BYC_DACOA
BIOB_CITER
ALL2_CARWA
ALL4_CARWA
ALL4_CARWA
ALL5_CARWA
ALL5_CARWA
ALL5_CARWA
ALL5_CARWA
ALL5_CARWA
ALL6_CARWA
ALL6_CARWA
ALL6_CARWA
ALL6_CARWA
ALL7_CYDPO
UC24_WAIZE
BOSI_HUWAN
RWO1_YEAAT
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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32
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No.
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Gaps

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28K ubiquitin-immunoreactive protein - inky cap (Coprinus cinereus) (fragment)
C;Species: Coprinus cinereus
C;Species: Coprinus cinereus
C;Species: Coprinus cinereus
C;Accession: A4376
R;Kanda, T.; Inoue, M.; Akiyama, M.;
Bicchinate 72, 355-359, 1990
A;Title: Purification and characterization of an ubiquitin-immuno-reactive protein local A;Reference number: A43766; MuID:91002724; PMID:1698461
A;Accession: A4376
A;Accession: A4376
A;Accession: A4376
A;Accession: A5376
A;Accession: A54
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5 IL 6
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Search completed: June 1, 2004, 11:19:23 Job time: 12.6667 secs

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C;Species: Staphylothermus marinus
C;Species: Staphylothermus marinus
C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C;Accession: S69237
C; Mol. Biol. 245, 385-401, 1995
C;Accession: Biol. 245, 385-401, 1995
C;Accession: S69237
C;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clacession: A60986
Ribrom, M.F.; Mellor, D.M.; Chadwick, V.S.
Ribrom, M.F.; Mellor, D.M.; Chadwick, V.S.
Bryerientia 45, 1097-1099, 1989
Bryerientia 45, 1097-1099, 1989
Bryerientia 45, 1097-1099, 1989
Bryerientia 45, 1097-1099, 1980
Bryerientia 45, 1097-1099, 1980
Bryerientia 45, 1097-1099, 1980
Bryerientia 45, 1097-1099, 1980
Bryerientia 45, 1097-1098
Bryerientia 45, 1097-1099
Bryerientia 45, 1097-1098
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NyAlternate names: delta-endotoxin
NyAlternate names: delta-endotoxin
Cispedias: Bacillus thuringiensis
Cipate: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
CiAccession: S14159
Riconvents, D.; Cherlet, M.; van Damme, J.; Lasters, I.; Lauwereys, M.
Bur. J. Blochem. 195, 631-635, 1991
A;Title: Two structural domains as a general fold of the toxic fragment of the Bacil
A;Reference number: S14087; MUD:9153300; PMID:1847865
A;Accession: S14159
A;Resesion: S14159
A;Residues: 1-6 <CON>
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C;Comment: This hexapeptide was the longest of several N-formyl oligopeptides report
F;I/Modified site: N-formylmethionine #status experimental
                                                                                                                                                                                                                                                                                                                                                      surface protein tetrabrachion heavy chain - Staphylothermus marinus (fragment)
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C;Species: Escherichia coli
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
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1 MATSS 5
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hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni) (fragm hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni) (fragm C; Species: Schistosoma mansoni)
C; Species: Sa-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 23-Jun-1993
C; Accession: A37114 #sequence_revision 0.H.; Wang, C.C.
J. Biol. Chem. 265, 13528-13332, 1990
A; Title: The hypoxanthine-guanine phosphoribosyltransferase of Schistosoma mansoni. Furt A; Reference number: A37114; MUID:90337955; PMID:2199439
A; Accession: A37114
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-5 < YUA.
C; Keywords: glycosyltransferase; pentosyltransferase
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34.5K structural protein - Leuconostoc oenos phage P32 (fragment)
34.5K structural protein - Leuconostoc oenos phage P32 (Stragment)
C,Species: Leuconostoc oenos Phage P32
C,Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: H44817
R;Arendt, BK.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A,Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: H44817
A;Molecule type: protein
A;Residues: 1-5 care.
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C;Species: Leuconostoc oenos phage P54
C;Species: Leuconostoc oenos phage P54
C;Accession: F44817
R;Arendt, B.K.; Lonvaud, A.; Hammes, W.P.
J;Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033; PMID:1748868
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A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70335)
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1 MATSS 5
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cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrior C; Species: mitochondrion Lampetra fluviatilis (river lamprey) C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001 (;Accession: T13892 Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G. Mol. Biol. Evol. 14, 807-813, 1997 A;Tillier, P.; Gachelin, G. A;Tillie: The main features of the craniate mitochondrial DNA between the ND1 and the A;Reference number: Z17775; MUID:97398704, PMID:9254918
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C;Species: Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Accession: E4-7ul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
C;Accession: E42364
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
J;Bacteriol, 173, 3364-3372, 1991
A;Fitcle: Salmonella typhimurium mutants defective in flagellar filament regrowth a A;Reference number: A42364; MUID:91258342; PMID:1646201
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: B60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolalin and partial characterization of major protein antigens in the c A;Reference number: A60274; MUID:91099989; PMID:1898889
A;Accession: B60274
A;Stetus: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>
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A,Molecule type: DNA
A,Residues: 1-3 <br/> <br/>A,Residues: 1-3 <br/> <br/>A)Cross-references: EMBL:Y09528; NID:g2340016; PIDN:CAA70721.1; PID:g4379123
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28.1%; Score 9; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indele
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A;Note: COI
C;Keywords: mitochondrion; oxidoreductase
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-5 < VOG>
A, Residues: 1-5 < VOG>
A, Cross-references: GB:M62408
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Cippecies: 29-Jun-1989 #text_change 16-Aug-1996
Cipate: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
Cipate: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
Cipate: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
Cipate: 23-Jun-1989 #sequence_revision of the Lorander, J.; Carson, D.; Sold R;Goni, F.R.; Chen, P.P.; Mcdinnis, D.; Aritel: Structural and idiotypic characterization of the Lorannes of human IgM autoanti A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Tetus: preliminary
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-7 <CON>
C;Keywords: heterotetramer; immunoglobulin
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                 34.5K structural protein - Leuconostoc oenos phage PZt11-15 (fragment)
C;Species: Leuconostoc oenos phage PZt11-15
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: B44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lyeogeny in Leuconostoc oenos
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: B44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55K structural protein - Leuconostoc oenos phage PAt5-12 (fragment)
C;Species: Leuconostoc oenos phage PAt5-12
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: D44817
C;Accession: D44817
A;Title: Lysogeny in Leuconostoc oenos
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: D44817
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.4%; Score 11; DB 2; Length 5; 60.0%; Pred. No. 2.8e+05; ative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Nolecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70340)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 10; DB 2; I
Pred. No. 2.8e+05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
E30608
Ig kappa chain V-III region (Gag) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.09
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LTISS 7
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RESULT 6

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June 1, 2004, 10:56:46; Search time 11.6667 Seconds (without alignments) 57.715 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                283366 segs, 96191526 residues
                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                        US-09-712-819C-1
32
1 FTLTISS 7
                                                                                                                                                                                          Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                  Run on:
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Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries PIR 78:\*
1: Dir1:\*
2: Dir2:\*
3: Dir3:\*
4: Dir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

branched-chain-ami
T-cell receptor be
34.5K structural profits
19 kappa chain V-I
Cytochrome-c oxida
flagellar protein
major protein anti
hypoxanthine phosp
34.5K structural proxanthine phosp
34.5K structural proxanthine phosp
34.5K structural proxanteace protein te
N-formyl oligopept
parasporal crystal
28K ubiquitin-immu
WHC H2-L antigen-protein - Esc
sex pheromone cAMI
sex protein 5507pullulanase (EC 3
globulin IV alpha
T-cell receptor be
T-cell receptor be Description SUMMARIES A40135 PT0644 PT0644 D44817 D44817 E530608 T123892 E60274 A448117 P44817 P44817 P64817 S14159 S14159 A5256 A32526 A32526 % Query Match Length DB

m RESULT

T-cell receptor be	glycogen phosphory		ribosomal protein	ribosomal protein	ribosomal protein	hypothetical prote		Ig heavy chain CRD	ell receptor	T-cell receptor be					
PT0697	A60521	I40698	I39964	139966	139965	T10954	I50385	PT0308	PT0596	PT0610	PT0597	PT0600	PT0729	PT0624	PT0686
0	73	(1)	N	N	7	0	71	71	7	Ŋ	7	Ŋ	Ŋ	N	0
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30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

## ALIGNMENTS

.,,,	RESULT 1	
	havorable chain-amino-acid transaminase (EC 2.6.1.42), mitochondrial - rat (f	2.6.1.42), mitochondrial - rat (fragment id aminotransferase, mitochondrial
	C. Date: 13-May-1992 #sequence_revision 13-May-1992 (C. Archest) nay-1992 #sequence_revision 13-May-1992	May-1992 #text_change 30-Sep-1993
	R.Hutson, S.M.; Wallin, R.; Hall, T.R. submitted to the Protein Sequence Database, Marc	, March 1992
	A, Molecule type: protein	
	A;Kesidues: 1-4 cn01> C;Keywords: aminotransferase; mitochondrion	п
•	Query Match 34.4%; Score 11; DB Best Local Similarity 66.7%; Pred. No. 2.8e Matches 2; Conservative 1; Mismatches	; DB 2; Length 4; . 2.8e+05; tches 0; Indels 0; Gaps 0;
	Qy 5 1SS 7	
	Db 1 VSS 3	
	RESULT 2	
	T-coell receptor beta chain V-D-J region (111-1G)	11-1G) - mouse (fragment)
	Cipecies: Mus.Musculus (Mouse Mouse) Cibate: 17-Jul-1992 #sequence_revision 17-Jul-1992 Cibatesion: DTACA44	Jul-1992 #text_change 30-May-1997
	R; Feeney, A.J.	•
	J. Exp. Med. 174, 115-124, 1991 A; Title: Junctional sequences of fetal T cell re	cell receptor beta chains have few N regio
	Prosos, MUID: 91277601	
	A; Status: translation not shown	
	A,Molecule type: mRNA A,Residues: 1-5 <fee></fee>	
	A;Experimental source: newborn thymus, strain BALB/ C;Keywords: T-ceil receptor	ain BALB/c
	Query Match 34.4%; Score 11; DB: Best Local Similarity 100.0%; Pred. No. 2.8 Matches 2; Conservative 0; Mismatches	, DB 2, Length 5, 5, 2.8e+05, cches 0, Indels 0, Gaps 0;
	Oy 1 FT 2	
	Db 4 PT 5	

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Sequence 198, Application US/09791378
Sequence 198, Application US/09791378
Sequence 198, Application US/09791378
Sequence 198, Application US/09791378
GENERAL INFORMATION:
APPLICANT: PEACEAN, Rajesh
TITLE OF INVENTION: SCHIZOPHRENIA
FILE REFERENCE: 9195-061-999
CURRENT APPLICATION NUMBER: US/09/791,378
CURRENT FILING DATE: 2001-02-23
FRICR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 677
SOFTWARE: Patentin version 3.0
SEQ ID NO 198
LENGTH: 7
Sequence 101, App Sequence 135, App Sequence 135, App Sequence 135, App Sequence 135, App Sequence 23, App Sequence 236, App Sequence 364, App Sequence 3542, App Sequence 344, App Sequence 131, App Sequence 356, App Sequence 356
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Patent No. US20020164664Ai
GENERAL INFORMATION:
APPLICANT: HIJVATY, John
APPLICANT: Briggman, Joseph
TITLE OF INVENTION: Detection and Treatment of Prostate Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.6%; Score 20; DB 9; Length 7; 42.9%; Pred. No. 1e+06;
                US-09-996-288-135

US-109-996-265-135

US-10-464-863-135

US-10-464-863-135

US-10-464-863-135

US-10-211-994-23

US-09-989-789-396

US-09-989-789-396

US-09-989-789-3544

US-09-989-789-3544

US-09-989-789-3544

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US-09-989-789-3544

US-09-996-288-96

US-09-996-288-16

US-09-996-288-16

US-09-996-288-18

US-09-996-265-35

US-09-996-265-35

US-09-996-265-35

US-09-996-265-35

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US-09-996-265-31

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-198
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YTFELSR 7
    RESULT 1
US-09-791-378-198
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Sequence 7, Appli
Sequence 205, App
Sequence 145, App
Sequence 145, App
Sequence 115, App
Sequence 115, App
Sequence 160, App
Sequence 164, Appl
Sequence 30, Appl
Sequence 30, Appl
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                                                                                                                               June 1, 2004, 11:18:42; Search time 34.6667 Seconds (without alignments) 56.387 Million cell updates/sec
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1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB_Pep:*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB_pep:*
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5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB_pep:*
7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB_pep:*
7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB_pep:*
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13: /cgn2_6/prodata/1/pubpaa/US108_PUBCOMB.pep:*
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16: /cgn2_6/prodata/1/pubpaa/US108_PUBCOMB.pep:*
17: /cgn2_6/prodata/1/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/prodata/1/pubpaa/US108_PUBCOMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-998-909-7
US-09-986-290-205
US-09-826-290-370
US-09-791-393-145
US-09-791-393-145
US-10-661100-105
US-10-264-309-145
US-10-264-309-146
US-10-264-309-146
US-09-996-286-164
US-09-996-286-164
US-09-996-286-164
US-10-162-497-78
US-10-162-497-78
US-10-161-833-164
                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                      1151071 segs, 279249464 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                              US-09-712-819C-6
33
1 FTLKISR 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0 Maximum DB seq length: 7
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Match
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Perfect score:
                                                                                                                                                                                                                                                                                                Scoring table:
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Sequence 145, Application US/09791393
Sequence 145, Application US/09791393
Sequence 145, Application No. US2030032200A1
GENERAL INFORMATION:
Herath, Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Pareth, Rajesh Bhikhu
APPLICANT: Pareth, Rajesh Bhikhu
APPLICANT: Pareth, Rajesh Bhikhu
APPLICANT: Pareth, Rajesh Bhikhu
APPLICANT: Porteins
TITLE OF INVENTION: Diagnosis and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder
TITLE OF INVENTION: UNDER: US/09/791,393
CURRENT FILING DATE: 2002-01-02
BARLIER PILING DATE: 2000-02-24
BARLIER FILING DATE: 2000-12-08
BARLIER FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 308
BARLIER FABEL FAB
                                                                          APPLICANT: Kimmel, Lida H.
APPLICANT: Barekh, Rajesh Bhikhu
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Potter, David M.
APPLICANT: Solber, Barich M.
APPLICANT: Silber, B. Michael
APPLICANT: Silber, B. Michael
APPLICANT: Stager, Thomas R.
APPLICANT: Sunderland, P. Trey
APPLICANT: White, Frost
APPLICANT: White, Frost
APPLICANT: White, Frost
APPLICANT: Williams, Stephen A.
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: Alzheimer's Disease
TITLE APPLICATION NUMBER: US 60/194,504
PRIOR APPLICATION NUMBER: US 60/194,504
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Best Local Similarity 42.9%; Pred. No. 1e+06;
Matches 3; Conservative 3; Mismatches 1; Indels
Friedman, David L.
Herath, Herath Mudiyanselage Athula Chandrasiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.6%; Score 20; DB 9; Length 7; 42.9%; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 492
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.9
Matches 3; Conservative
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; ORGANISM: homo sapien
US-09-791-393-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: homo sapien
US-09-826-290-370
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US-09-791-393-145
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Batent No. US20020164668A1

GENERAL INFORMATION:
APPLICANT: Durham, L.Kathryn
APPLICANT: Priedman, David L.
APPLICANT: Friedman, David M.
APPLICANT: Rimmel, Lidath Mudiyanselage Athula Chandrasiri
APPLICANT: Rimmel, Lidath Mudiyanselage Athula Chandrasiri
APPLICANT: Rimmel, Lidath Mudiyanselage Athula Chandrasiri
APPLICANT: Rimmel, Lidath Michael
APPLICANT: Ringer David M.
APPLICANT: Ridger Thomas R.
APPLICANT: Ridger Thomas R.
APPLICANT: Sudderland, P. Trey
APPLICANT: Sudderland, P. Trey
APPLICANT: Sudderland, P. Trey
APPLICANT: White, Frost
APPLICANT: White, Frost
APPLICANT: Williams, Stephen A.
TITLE OF INVENTION: USes Therefor, Including Diagnosis and Treatment of
TITLE OF INVENTION: Alzheimer's Disease
TITLE REFERENCE: 2572-1-001 N2
CURRENT FILING DATE: 2000-04-30
PRIOR FILING DATE: 2000-04-30
PRIOR FILING DATE: 2000-04-30
PRIOR PLING DATE: 2000-04-30
PRIOR FILING DATE: 2000-04-30
PRIOR PLING DATE: 2000-04-30
PRIOR PLING DATE: 2000-04-30
PRIOR PLING DATE: 2000-04-30
SOFTWARE FASED for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20; DB 9; Length 7; Pred. No. 1e+06; 1; Indels 3; Mismatches 1; Indels
                   FILE REFERENCE: MTP-027
CURRENT APPLICATION NUMBER: US/09/998,909
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/250,284
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATCHIN VERSION 3.0
SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.9
Matches 3; Conservative
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CORGANISM: Homo sapiens
US-09-998-909-7
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; ORGANISM: homo sapien
US-09-826-290-205
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1 FTFEYSR 7
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1 YTFELSR 7
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US-09-826-290-370
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APPLICANT: STIGER, THOMAS R.
APPLICANT: STIGER, THOMAS R.
APPLICANT: STIGER, THOMAS R.
APPLICANT: WILLIAMS, P. TREY
APPLICANT: WILLIAMS, STEPHEN A.
TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
FILE REPERENCE: POA-002.01
FILE REPERENCE: 2002-10-03
PRIOR APPLICATION NUMBER: 60/326,708
PRIOR PLING DATE: 2001-10-03
PRIOR PLING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 491
SEQ ID NO 131
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR, TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE FILE REFERENCE: POA-002.01
CURRENT APPLICATION NUMBER: US/10/264,309
CURRENT FILING DATE: 2002-10-03
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; Sequence 131, Application US/10264309; Publication No. US20040022794A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 460, Application US/10264309
Publication No. US20040022794A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-10-03
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ROHLEP, CHRISTIAN
SILBER, B. MICHAEL
SNYDER, PETER J.
SOARES, HOLLY D.
STICER, THOMAS R.
SUNDERLAND, P. TREY
TOWNSEND, ROBERT R.
WHITE, W. PROST
WILLIAMS, STEPHEN A.
                                                                                          FRIEDMAN, DAVID L.
HERATH, HERATH
KIMMEL, LIDA H.
PAREKH, RAJESH B.
POTTER, DAVID M.
ROHLFF, CHRISTIAN
SILBER, B. MICHAEL
SINDER, PETER J.
SOARES, HOLLY D.
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Best Local Similarity 57.1
Matches 4; Conservative
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CORGANISM: Homo sapiens
US-10-264-309-131
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1 FTFEYSR 7
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PAREKH,
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US-10-264-309-460
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                                                                                                     SAPELICANT: Herath, Herath Mudiyanselage Athula Chandrasiri,
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Rohlff, Christian
APPLICANT: Terrett, Jonathan Alexander
APPLICANT: Terrett, Jonathan Alexander
TITLE OF INVENTION: Proteins, Genes and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: and Unipolar Depression
TITLE OF INVENTION: and Unipolar Depression
FILE REFERENCE: 2543-1-001 N2
CURRENT APPLICATION NUMBER: GB 0004412.3
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 308
SOFTWARE: FastSEQ for Windows Version 4.0
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| Publication No. US20040072261A1
| GENERAL INFORMATION:
| APPLICANT: INFORMATION:
| TITLE OF INVENTION: Nethod for the Diagnosis and Differential Diagnosis of
| TITLE OF INVENTION: Neurological Diseases
| FILE REFERENCE: 11362.0038.NPUSO1;
| CURRENT APPLICATION NUMBER: US/10/601,100
| CURRENT APPLICATION NUMBER: US/203-66-20
| PRIOR PILING DATE: 2003-66-21
| PRIOR PILING DATE: 2002-06-21
| PRIOR PILING DATE: 2002-06-21
| PRIOR PILING DATE: 2002-06-31
| PRIOR PILING DATE: 2002-06-31
| PRIOR PILING DATE: 2002-07-17
| NUMBER OF SEQ ID NOS: 113
| SEQ ID NO 105
| LENGTH: 7
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                                      Sequence 145, Application US/09791389
Publication No. US20030032773A1
GENERAL INFORMATION:
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Best Local Similarity 42.9
Matches 3; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
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US-10-601-100-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT CAGANISM: homo sapien US-09-791-389-145
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1 YTFELSR 7
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Sequence 164, Application US/10461863
Publication No. US20040018200A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Oliver, Cynthia
APPLICANT: Allan, Christian
APPLICANT: Chang, Stephen
APPLICANT: NUMBER: US/10/461,863
CURRENT APPLICATION NUMBER: US/10/461,863
PRIOR APPLICATION NUMBER: 60/388,920
PRIOR FILING DATE: 2002-06-14
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APPLICANT: Chen, H.

APPLICANT: Chen, H.

TITLE OF INVENTION: HETHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
FILE REFERENCE: 7853-138
FILE REFERENCE: 7853-138
FILE REPERENCE: 7853-138
CURRENT FAPILICATION NUMBER: US/10/162,497
CURRENT FILING DATE: 2000-09-07
PRIOR PELING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
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Pred. No. 1e+06;
2; Mismatches 1; Indels
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50.0%;
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 50.0
Matches 3; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-497-78
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; ORGANISM: Homo sapiens
US-10-461-863-164
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2 YTMKYS 7
                  TMKLS 6
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APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Lealie, Johnson
TITLE OF INVENTION: Methods of Adminetering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
TITLE OF INVENTION: and Treatment
CURRENT APPLICATION NUMBER: US/9996,265
CURRENT APPLICATION NUMBER: US/9996,265
CURRENT PILING DATE: 2001-11-28
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 164
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Young, James
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Lesia, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT PILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 164
LENGTH: 74
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Pred. No. 1e+00
3; Mismatches
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Publication No. US20030091584A1
GENERAL INFORMATION:
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Patent No. US20020177126A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Version 2.1 SEQ ID NO 460
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Best Local Similarity 60.00
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Best Local Similarity 42.9
Matches 3; Conservative
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; ORGANISM: Homo sapiens
US-09-996-288-164
                                                                                       TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-460
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US-09-996-265-164
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Best Local Similarity
Matches 3; Conserv
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1 YTFELSR 7
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US-09-996-288-164
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US-09-996-265-164
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Job time : 35.6667 secs
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Publication No. US20030114650A1

GENERAL INFORMATION

APPLICANT: Cheung, Ambrose

APPLICANT: Cheung, Adar

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN

FILE REFREENCE: DC-0199

CURRENT APPLICATION NUMBER: US 60/261, 233

FRIOR APPLICATION NUMBER: US 60/261, 607

PRIOR PILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

SOUTHARE: PARENTER TON NUMBER: US 60/289, 601

PRIOR FILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 34

SOUTHARE: PARENTER: PARENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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US-10-105-930-39
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Search completed: June 1, 2004, 11:31:24

3 LKISR 7

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36, Appl

336, Appl

55, Appl

17, Appl

17, Appl

66, Appl

41, Appl

41, Appl

41, Appl

41, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lidenstein, Henri
APPLICANT: Lidenstein, Henri
APPLICANT: Lyons, David
APPLICANT: Wurfel, Mark
APPLICANT: Wright, Samuel
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oake
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.6%; Score 20; DB 1; Length 7; 57.1%; Pred. No. 3e+05; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,619
US-08-305-871A-17
US-08-388-822A-1
US-08-134-231C-36
US-08-126-160-36
US-09-040-216-55
US-09-040-216-55
US-09-511-632-17
US-09-511-451-17
US-09-611-451-17
US-09-611-451-17
US-08-135-17
US-08-135-17
US-08-136-17
US-08-222-619-21
US-08-222-619-21
US-08-222-619-21
US-08-222-619-21
US-08-222-614-6
US-08-222-614-6
US-08-175-069A-41
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PCT-US95-04075-8
S Sequence 8, Application PC/TUS9504075
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08222619; Patent No. 5652352; GENERAL INFORMATION:
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Best Local Similarity 57.1
Matches 4; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FILKISR 7
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Sequence 3544, Ap
Sequence 72, Appl
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                                                                                                              1, 2004, 11:13:51 ; Search time 13.6667 Seconds (without alignments) 26.443 Million cell updates/sec
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Sequence 78,
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'GgDZ_6/ptodata2/jaa/5A_COMB.pep:*
'GgDZ_6/ptodata2/jaa/5B_COMB.pep:*
'GgDZ_6/ptodata2/jaa/6A_COMB.pep:*
'GgDZ_6/ptodata2/jaa/6B_COMB.pep:*
'GgDZ_6/ptodata2/jaa/PCTUS COMB.pep:*
'GgDZ_6/ptodata2/jaa/PCTUS COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                      389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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33
1 FTLKISR 7
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Match Length
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encoded modified polypeptides with target substrates.
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Patent No. 6342351

GENERAL INFORMATION:
APPLICANT: Chen, H.
APPLICANT: Chen, H.
APPLICANT: Chen, M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
ITTLE OF INVENTION: METHODS AND CHROMSOME-18P RELATED DISORDERS
FILE REFERENCE: 7853-138

CURRENT APPLICATION NUMBER: US/09/268,992

CURRENT FILING DATE: 1999-01-22

BARLIER PELING DATE: 1999-01-22

BARLIER PELING DATE: 1999-10-28

BARLIER PELING DATE: 1999-01-28

BARLIER PELING DATE: 1998-10-36

BARLIER PELING DATE: 1998-03-16

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 3.0

TYPE: PRI
TYPE: PRI

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                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
         TITLE OF INVENTION: encoded modified polypept:
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIPICATION 435
FILING DATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/039,501
FILING DATE:
APPLICATION NUMBER: US 07/602,158
FILING DATE: 22-0CT-1990
ATTORNEY/AGRAT INFORMATION:
NAME: TECCATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-53469/RFT
TELECOMUNICATION INFORMATION:
TELEPRONE: (415) 398-3249
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Pred. No.
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-346-333-24
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Fatent No. 5677153
GENERAL INFORMATION:
APPLICANT: Botstein, David
APPLICANT: Palzkill, Timothy
ITLE OF INVENTION: Methods for modifying DNA and for
TITLE OF INVENTION: detecting effects of such modification on interaction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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;Patent No. 5252328
; Patent No. FAULDS, DARYL;VISHOOT, MIMI;BROOKS, EMILY
; TITLE OF INVENTION: MYCOFLASMA HYOPNEUMONIAE ANTIGEN AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20; DB 5; Length 7; Pred. No. 3e+05;
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Pred. No. 3e+05;
); Mismatches 1; Indels
APPLICANT: AMGEN INC.
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SECURNOES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC
                                                                                                            ADDRESSEE: Augen Center, Patent Operations/RRC STREET: 1840 DeHavilland Drive CITY: Thousand Oaks STATE: California COUNTRY: U.S.
ZIP: 91320-1789
COMPUTER READABLE FORM: MEDIUM TYPE: IBM PC COMPATER: IBM PC COMPATER: IBM PC COMPATER: OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04075
FILING DATE:
CLASIFFCATION:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/335,726
FILING DATE: 07-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 30,130
FILING DATE: 26-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FTLKISR 7
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1 FTFEYSR 7
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US-08-346-333-24
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Gaps

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PGT-USES - 07506-24

PGT-USES - 04 Application PC/TUS9107506

Sequence 24, Application PC/TUS9107506

GENERAL INFORMATION:
APPLICANT: Belstein, David
APPLICANT: Belstein, Timothy
TITLE OF INVENTION: Methods for modifying DNA and for
TITLE OF INVENTION: encoded modified polypeptides with target substrates.
TITLE OF INVENTION: encoded modified polypeptides with target substrates.
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STRATE: California
COUNTY: USA
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                            Score 18; DB 4; Length 7; Pred. No. 3e+05; 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUDNIKE: USEN

ZIP: 94111

COMPUTER READABLE FORM:
MEDIIOM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: POCCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN RC-DOS/MS-DOS
SOFTWARE: PACENTIN RC-DOS/MS-DOS
SOFTWARE: PACENTIN RC-DOS/MS-DOS
FILING DATE: 19911021
CLESSIFICATION NUMBER: PCT/US91/07506
FILING DATE: 19911021
CLESSIFICATION: Richard F.
REFERENCY/DOCKET NUMBER: PF-53469-PC/RPT
TELEPHONE: (415) 398-3249
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
LENGTH: 7 amino acids
TTYPE: AMINO ACID
COMPUTER FORM SID ID
COMPUTED TO SEQ ID
COMPUTED T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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US-09-174-060-17
US-09-174-060-17
Sequence 17, Application US/09174060
Patent No. 5989554
GENERAL INFORMATION:
APPLICANT: Knuth, Mark W
APPLICANT: Haak-Frendscho, Mary
APPLICANT: Shultz, John W
APPLICANT: Lealey, Scott A
APPLICANT: Lealey, Scott A
APPLICANT: Villars, Catherine E
                                                                                                                        Query Match
Best Local Similarity 60.0%;
Matches 3, Conservative
            ; ORGANISM: Escherichia coli
US-08-753-750B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                      1 FTLKI S
                                                                                                                                                                                                                                                                                                                                                     1 FTLSV 5
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| Patent No. 6610506
| GENERAL INFORMATION|
| GENERAL INFORMATION|
| APPLICANT: Lo, Regist Y.C.
| APPLICANT: Schryvers, Anthony B.
| APPLICANT: Potter, Andrew A.
| TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME FILE REPRENCE: A37762 021645.0105
| TITLE OF INVENTION: PASTEURELLA AND VACCINES CONTAINING THE SAME FILE REPRENCE: A37762 021645.0105
| CURRENT APPLICATION NUMBER: US 06/05509
| PRIOR APPLICATION NUMBER: 60/008,569
| PRIOR FILING DATE: 1995-12-01
| PRIOR FILING DATE: 1995-12-01
| PRIOR FILING DATE: 1995-12-01
| NUMBER OF SEQ ID NOS: 68
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 7
| TYPE: PRI
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Patent No. 6399762

GRERRAL INFORMATION:
APPLICANT: Chen, H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND TREATING CHROMOSOME-18P RELATED DISORDERS;
TILE REFERENCE: 7883-138

FILE REFERENCE: 7883-138

FRICK APPLICATION NUMBER: US/09/68,992

FRICK PALING DATE: 1999-03-16

FRICK PILING DATE: 1999-03-16

FRICK PILING DATE: 1999-01-22

FRICK PILING DATE: 1998-10-28

FRICK PILING DATE: 1998-10-65

FRICK FILING DATE: 1998-06-05

FRIC
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0
                                                                                                                                                                                                   1; Indels
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Pred. No. 3e+05;
2; Mismatches 1; Indels
                                                                                                                        Length 7;
                                                                                                                    3; DB 4;
                                                                                                                Score 18; DB 4
Pred. No. 3e+05
2; Mismatches
                                                                                                            54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.5%;
                                                                                                            Query Match
Best Local Similarity 50.0
Matches 3, Conservative
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Best Local Similarity 50.0.
; ORGANISM: Homo sapiens
US-09-268-992-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
JS-09-657-474-78
                                                                                                                                                                                                                                                                  1 FTLKIS 6
                                                                                                                                                                                                                                                                                                               :|:| |
2 YTMKYS 7
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2 YTMKYS 7
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Patent No. 6069230
GENERAL INFORMATION:
APPLICANT: Knuth, Mark W
APPLICANT: Haak-Frendscho, Mary
APPLICANT: Shiltz, John W
APPLICANT: Leslex, Scott A
APPLICANT: Villars, Catherine B
TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE
TITLE OF INVENTION: PURIFICATION, PURIFICATION, PURIFICATIONS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ross & Stevens, S.C.
STREET: Louth Pinckney St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 51.5%; Score 17; DB 3; Length 7; Best Local Similarity 60.0%; Pred. No. 38+05; Matches 3; Conservative 2; Mismatches 0; Indels
                                CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION 475:
APPLICATION NUMBER: 6B 9225453.1
FILING DATE: 04-DEC-1992
PRICH PAPLICATION NUMBER: 6B 9300816.7
FILING DATE: 10-MAY-1993
PRIOR APPLICATION NUMBER: EP 93303614.7
FILING DATE: 10-MAY-1993
PRIOR APPLICATION NUMBER: EP 93303614.7
FILING DATE: 10-MAY-1993
PRIOR APPLICATION NUMBER: 6B 9319969.3
FILING DATE: 10-MAY-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: 6B 9412147.2
FILING DATE: 17-UNM-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: 6CT/GB94/02662
FILING DATE: 05-DEC-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: 6CT/GB94/02662
FILING DATE: 05-DEC-1994
PRIOR APPLICATION NUMBER: 6CT/GB94/02662
FILING DATE: 05-DEC-1994
PRIOR APPLICATION NUMBER: 6CT/GB94/02662
FILING DATE: 05-DEC-1994
PRIOR APPLICATION NUMBER: 6CT/GB94/02662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 2811/33259
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
INFORMATION FOR SEQ. ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/448,418
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
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TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE
TITLE OF INVENTION: PUBLIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR
TITLE OF INVENTION: IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: ROSS & Stevens, S.C.
STREET: 1 South Pinckney St.
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 69 Application US/08654623

Patent No. 610884

GENERAL INPORMATION:
APPLICANT: Griffiths, Andrew D
APPLICANT: Holliger, Kaspar-Philipp
APPLICANT: Hisch, IAch, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.5%; Score 17; DB 2; Length 7; 75.0%; Pred. No. 3e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
APPLICATION DATA:
APPLICATION NUMBER: US/08/654,623
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/174,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34506.024
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/338,382
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Sara, Charles S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 34506.03
TELEPRANE: 608-257-353
TELEPRANE: 608-257-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: 608-25/->...
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.03
Matches 3, Conservative
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STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-174-060-17
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STREET: boc.
CITY: Chicago
                                                                                                                                                                                                                                                            CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-654-623-69
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ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
       NAME: Fitting, Thomas
REGISTRATION WUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INPORMATION:
TELEPHONE: (619) 784-2937
TELEPHONE: (619) 784-2939
INPORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/09611451; Patent No. 6395275; GENERAL INFORMATION: APPLICANT: Barbas, Carlos F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (619) 784-93
INPORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: La Jolla
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                         5 amino acids
                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-591-632-23
                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 FTLQ 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Barton, Dennis R.
APPLICANT: Burton, Dennis R.
APPLICANT: Burton, Dennis R.
APPLICANT: Burton, Burton, Dennis R.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNOBERICIENCY VIRUS
NUMBER OF SECURNES: 92
CORRESPONDENCE ADDRESS: 92
CORRESPONDENCE ADDRESS: Patent Counsel
ADDRESSEE: Patent Counsel
ADDRESSEE: Patent Counsel
ADDRESSEE: Patent Counsel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.5%; Score 17; DB 3; Length 7; 75.0%; Pred. No. 3e+05; tive 1; Mismatches 0; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIP: 92037

ZIP: 92037

ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PEtentin Release #1.0

APPLICATION UNMERE: US/08/591,632
FILING DATE: 19-CCT-1994
APPLICATION NUMBER: PCT/US94/11907
FILING DATE: 19-CCT-1994
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-CCT-1994
APPLICATION NUMBER: US 08/308,841
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: US 08/33,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/133,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-CCT-1993
APPLICATION NUMBER: 118-L1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/08591632 Patent No. 6261558
                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
GLASSIFICATION: 435
ATTORNEY, AGENT INPORMATION:
NAME: Sara, Charles S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 34506
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAK: 608-257-9175
INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
LANGHA: 7 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1055c
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FTLK 4
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Lerner, Righard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
ANTIBODIES TO HUMAN IMMUNOBERICIENCY VIRUS
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of Patent Counsel STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8 Query Match

48.5%; Score 16; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/99/611,451
FILING DATE: 06-Jul-200

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 20-SEP-1994
APPLICATION NUMBER: US 08/33,619
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-CGT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fiting, Thomas
REGISTATION NUMBER: 34,163
REGISTATION NUMBER: 15-GCT-1993
ATTORNEY/AGENT THORMATION:
NAME: Fiting, Thomas
REGISTATION NUMBER: 15R1 332.3
TELECOMMUNICATION:

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2 TAKVS 6
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                                                                                                                                                 Gaps
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Sequence 5, Application US/07717331F
Patent No. 5484905
GENERAL INFORMATION:
APPLICANT: June Narallah; Michael Nasrallah, and Joshua
APPLICANT: Stein
TITLE OF INVENTION: A Receptor Protein Kinase Gene
TITLE OF INVENTION: Brocded At The Self-Incompatability Locus
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
                                                                            Score 16; DB 4; Length 5; Pred. No. 3e+05;
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Pred. No. 3e+05;
1; Mismatches 0; Indels
                                                                                                                                       1; Mismatches
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ZIP: 06611
COMPUTER READABLE FORM:
MADIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/17,331F
FILING DATE: June 19th 1991
CLASSIFICATION NUMBER: US/07/17,331F
FILING DATE: June 19th 1991
CLASSIFICATION NUMBER: US/07/17,331F
FILING DATE: June 19th 1991
CLASSIFICATION NUMBER: 25,824
FELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
                                                                        48.5%;
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                                                           Query Match
Best Local Similarity 75.0
Matches 3, Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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MOLECULE TYPE: peptide
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US-09-611-451-23
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US-08-757-425B-44

'Sequence 44, Application US/08757425B

Sequence 4500660

'BENERAL INFORMATION:

APPLICANT: Fastrez, Jacques

TITLE OF INVENTION: Chimeric Target Molecules Having A Regulatable Activity

TITLE OF INVENT APPLICATION NUMBER: US/08/757,425B

CURRENT APPLICATION NUMBER: US/08/757,425B

NUMBER OF SEQ ID NOS: 78

SOFTWARE: Patentin version 3.1

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; IENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FRAUTE:
; OTHER INFORMATION: Mimetope
US-08-757-425B-44

Query Match
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps

Qy 2 TLKIS 6
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| Db 2 TAKUS 6

Search Completed: June 1, 2004, 11:20:18
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PT0518
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A30812
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PT0669
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Best Local Similarity 50.0
Matches 2; Conservative
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T-cell receptor be
T-cell receptor be
surface protein te
dnaA protein - Pse
N-formyl oligopept
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phosphotransferase
18K protein 5507 -
neuromodulatory pe
neuromodulatory pe
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22K guperhelical D
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28K ubiquitin-immu
neuropeptide TE-6
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glycoprotein compo
                                                                                                                                                                                                                                                                                                                           T-cell_receptor be ribosomal protein
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ribosomal protein
                                                                                                                                                                                                                                                                                                   DNA topoisomerase
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                                                  (without alignments)
51.795 Million cell updates/sec
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                                           2, 2004, 18:54:42 ; Search time 13 Seconds
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                 283366 segs, 96191526 residues
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Listing first 45 summaries
                               - protein search, using sw model
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A44955
S11127
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A60521
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Gapop 10.0 , Gapext 0.5
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Match Length
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1: pir1:*
2: pir2:*
3: pir3:*
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Perfect score:
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aglycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (freglycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (5/species: Bos primiganius taurus (cattle)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accesion: E48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
A;Reference number: A48394; MUID:93250576; PMID:8485470
A;Accession: E88394
A;Nolecule type: protein
A;Residues: 1-7 <AMT>
A;AResidues: 1-7 <AMT>
A;Residues: 1-7 <AMT>
A;Residues: 1-7 <AMT>
A;Residues: 1-7 <AMT>
A;AResidues: 1-7 <AMT>
A;AResidues
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c)Species: Oryctolagus cuniculus (domestic rabbit)
c)Species: Oryctolagus cuniculus (domestic rabbit)
c)Species: Oryctolagus cuniculus (domestic rabbit)
c)Species: Oct-1992 #sequence revision 30-Oct-1992 #text_change 13-Sep-1996
C)Accession: B26206, A26206
B;Larner, J; Sanger, F.
J, Mol. Biol. 11, 491-500, 1965
A;Title: The amino acid sequence of the phosphorylation site of muscle uridine diphosphocy A;Reference number: A26206
A;Accession: B26206
A;Molecule type: protein
A;Residues: 1-6 < LAR>
A;Experimental source: muscle
A;Note: 1-9-1 was also found
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;4/Binding site: phosphate (Ser) (covalent) #status experimental
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choline oxidase (E
pills protein. - Esc
sex pheromone CGP1
phosphonoacetaldeh
omega-gliadine 1,
Ig heavy chain CRD
Ig kappa chain V-I
T-cell receptor be
peptidylglycine mo
carnocin U149 - Ca
MHC H2-L antigen -
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22K Superhelical DNA-binding protein - Escherichia coli (fragment)
CjSpecies: Bscherichia coli
CjSpecies: Bscherichia coli
CjSpecies: Bscherichia coli
CjAccession: A6100
CjAccession: A
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A;Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete ge A;Reference number: S19630; MUID:92144363; PMID:1736962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A.Reference number: PT0509; MUID:91277601; PMID:1711558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Streptomyces griseus
C.Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 06-Jun-1997
C.Accession: S19630
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Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.3%; Score 11; DB 2; Le
100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
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A;Nolecule type: mRNA
A;Residues: 1-5 < FEBA
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor
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Pred. No. 2.8e+05;
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66.7%;
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Best Local Similarity 66...
'haa 2; Conservative
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A;Status: translatio
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*Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
                                                                                                                                                 DNA topoisomerase II alpha - Chinese hamster (fragment)

C;Species: Cricetulus griseus (Chinese hamster)

C;Species: OcJul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C;Accession: 148086

R;Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.

J. Biol. Chem. 270, 22850-25858, 1995

A;Title: Molecular cloning and characterization of the promoter for the Chinese hamster

A;Reference number: 148086; MUID:96025684; PMID:7592770
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A;Cross-references: BMBL:U34196; NID:g1041231; PIDN:AAC52315.1; PID:g1041232
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A;Experimental source: ssp. Hamburger Schnitt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        major fat-globule membrane protein GP 55 - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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A;Molecule type: protein
A;Residues: 1-7 <MATA:
A;Experimental source: milk
A;Experimentel source milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           II-like sequences.
A;Reference number: A48394; MUD:93250576; PMID:8485470 A;Status: praliminary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7 <RES>
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Best Local Similarity 50.0
Matches 2; Conservative
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neuromodulatory peptide Wwamide-2 - giant African snail
C;Species: Achatina fulta (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: 833245
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
A;Minakata, 1933, 104-108, 1993
A;Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (fragn C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Date: 15-Uun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: T13892
R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol: 14, 807-813, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuromodulatory peptide Wwamide-1 - giant African snail
C;Species: Acharina fulica (giant African snail)
C;Dacei 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S3324
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
A;Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of A;Reference number: S33244; MUID:93265912; PMID:8495720
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submitted to JIPID, April 1993
A;Reference number: PS0206
A;Accession: PS0254
A;Molecule type: protein
A;Residues: 1-7 < TSU>
A;Experimental source: leaf, chloroplast, strain Nihonbare
A;Note: molecular weight 18K, pI 4.4
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIN>
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A,Molecule type: protein
A,Residues: 1-7 <MIN>
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A. Title: Purification and characterization of glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)

N. Alternate names: glycogen phosphorylase b
C. Species: Liza ramada
C. Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
C. Accession: A6021
C. Accession: A6021
C. Bananate, L. B 95, 295-301, 1990
A. Title: Purification and characterization of glycogen phosphorylase B from skeletal musch Reference number: A6021; MUID: 90227907; PMID: 2109669
A. Accession: A6051
A. Molecule type: protein
A. Accession: A6051
A. Molecule type: protein
C. Superfamily: glucan phosphorylase
C. Reywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F: 3/ Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
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C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C;Accession: P50254
R;Tsugita, A.
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A;Accession: B33127
A;Status: preliminary
A;Molecule type: DNA
A;Rerose-references: GB:M38416; NID:9155142; PIDN:AAA98418.1; PID:9155144
C;Keywords: phosphotransferase
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                                                                                                                       Query Match 33.3%; Score 11; DB 2; Length 7; Best Local Similarity 40.0%; Pred. No. 2.8e+05; Matches 2; Conservative 3; Mismatches 0; Indels
C;Superfamily: Escherichia coli ribosomal protein L30
C;Keywords: protein biosynthesis; ribosome
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3 LKITO 7
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5 OIS 7
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Hadellar procein filk - Salmonella typhimurium (fragment)

Cispecies: Salmonella typhimurium

Cispecies: Salmonella typhimurium

Cispecies: Salmonella typhimurium

Cispecies: Salmonella typhimurium

Rivogler, A.P.; Homman, M.; Irikura, V.M.; Macnab, R.W.

A. Bacteriol. 173, 3564-3572, 1991

A. Bacteriol. 173, 3564-3572, 1991

A. Firtle: Salmonella typhimurium murants defective in flagellar filament regrowth and seq A. Stetus: preliminary

A. Soloceuse type: DNA

A. Soloceuse type: DNA

A. Stetus: Carlonian Salmonella Salmonell
Title: The main features of the craniate mitochondrial DNA between the ND1 and the CO1 Reference number: Z17775; MUID:97389704; PMID:9254918
Accession: T13892
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-3 < DEL>
Cross-references: EMBL:Y09528; NID:g2340016; PIDN:CAA70721.1; PID:g4379123
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Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
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27.3%; Score 9; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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Job time: 14 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,Genome: mitochondrion
,Note: COI
,Keywords: mitochondrion; oxidoreductase
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SEQUENCE, AND MASS SPECTROMETRY.
TISSUB—Skin secretion:
Steinborner. S.T., Waugh R.J., Bowie J.H., Gao C.,
Steinborner. S.T., Wallace J.C.,
"The ructure of new peptides from the Australin red tree frog
Lintoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=WS;
MEDLINE=98291870; PubMed=9629918;
MEDLINE=98291870; PubMed=9629918;
Flandsrud R., Sk-Fladal L.;
Flandsrud R., Sk-Fladal L.;
Flandsrud St., St., St., Sk-Fladal L.;
Flandsrud L., MISCELLANGUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.

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28-FBE-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
11-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation update)
11-Intoria rubella (Desert tree frog).
12-Intoria rubella (Desert tree frog).
13-Intoria rubella (Desert tree frog).
14-Intoria rubella (Desert tree frog).
15-Intoria rubella (Desert tree frog).
16-Intoria rubella (Desert tree frog).
16-Intoria rubella (Desert tree frog).
17-Intoria rubella (Desert tree frog).
18-Intoria rubella (Desert tree frog).

                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Unknown protein CP & from 2D-page (Fragment).
Clostridium pasterrianum.
Bacteriais Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
P011162
P58706
P13071
P13071
P821099
P821000
P821000
P821000
P821000
P820070
                                                                                                                                                                 P13736
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                                                                                                                                                                                                                                                                                       6 AA.
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                                                                         LITRU
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P81351;
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   SEQUENCE
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RE31 LITRU
ID RE31 LIT
AC P82072;
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P81158 cydia pomon
P3189 ascaris suu
P82071 litoria rub
P25154 oryctolagus
P41491 locusta mig
P38641 mus musculu
P38920 achatina fu
P35920 achatina fu
P35920 hirudo medi
P42563 hirudo medi
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P42563 hirudo medi
P42561 hirudo medi
P58705 anthopleura
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carcinus ma
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P82073 litoria rub
P82101 litoria rub
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P35921 achatina fu
P38639 mus musculu
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P82072 litoria rub
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                                                                                                    June 2, 2004, 18:47:58 ; Search time 10 Seconds (without alignments) 36.449 Million cell updates/sec
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P16101
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               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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RE32_LITRU
WMA1_ACHFU
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WWA3_ACHFU
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Maximum Match 100%
Listing first 45 summaries
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length: 7
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Match
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Perfect score:
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Maximum DB
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Query Match

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Achatina fulica (Giant African snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Fulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatina.
NCBI_TaxID=6530;
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Bukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBI_TaxID=6530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minakata H., Ikeda T., Muneoka Y., Kobayashi.M., Nomoto K.; "Wwanide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";
Litori electrica. Comparison with the skin peptides from Litoria
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7 AA; 834 MW; 6DD05B076B0B5030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 7 AMIDATION,
7 AA; 993 MW; 7362D5B69B041310 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
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01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                           TISSUE=Ganglion;
MEDLINE=93265912; PubMed=8495720;
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P35921;
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ID WWAI ACHFU
AC P35919;
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SEQUENCE
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Wabhitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;
Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Skin secretion,
Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
Pelodryadinae, Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Litoria rubella (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia; Hyloidea, Hylidae;
Pelodryadinae, Litoria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aust. J. Chem. 52:639-645(1999).
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
         -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
                                                                             -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-1- MASS SPECIFICITY: MW=655; MTHOD=FAB.
Amphibian defense peptide; Amidation.
MOD RES
SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-in-phibian defense peptide 71h9C9C862A00000 CRC64;
SEQUENCE 5 AA: 570 MM; 71h9C9C862A00000 CRC64;
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                                                                                                                                                                                                                                                        Match 33.3%; Score 11; DB 1; Le Local Similarity 100.0%; Pred. No. 1.4e+05; es 2; Conservative 0; Mismatches 0;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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Last annotation update)
                                                              -1- SUBCELLULAR LOCATION: Secreted.
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28-FEB-2003 (Rel. 41, Last sequ
10-OCT-2003 (Rel. 42, Last anno
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ID _EIOS_LITRU
AC P82101;
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P82073;
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UF01 MOT P38639; RESULT 7 UF01 MOUSE

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oxidase from Alcaligenes 8p.";
J. Biochem. 88:197-203(1980).
-!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-PEB-1991 (Rel. 17, Last annotation update)
Sex pheromone cAM373 (Clumping-inducing agent) (CIA).
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C., White B.A., An F.Y., Clewell D.B., Suzuki A.; "Isolation and structure of the Streptococcus faecalis sex pheromone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIJUNE-81006769; PubMed-6997283;
Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
"Identification and properties of the prosthetic group of choline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alcaligenes sp.
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
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-i- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
PIR; A25269; A25269.
Pheromone. 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;
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-!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS HARBORING PAM373.
                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                          27.3%; Score 9; DB 1; Length 7; llarity 100.0%; Pred. No. 1.4e+05; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;
        790 MW; 72C9D2C731B2C740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
Choline oxidase (EC 1.1.3.17) (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alcaligenaceae; Alcaligenes.
NCBI_TaxID=512;
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Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                     Local Similarity
     7 AA;
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P16101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIA ENTFA
P11932;
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        SEQUENCE
                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                           Best Loc
Matches
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Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=9008313; Pubmed=3139658; MEDLINE=9008313; Pubmed=3139658; Medit M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M., Adsit J.C., Dunny G.M., Suzuki A.; Sizuki C. C. C. Sizuki A.; Sizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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01-OCT-1994 (Rel. 30, Last sequence update)
15-WAR-2004 (Rel. 43, Last annequence update)
Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
                                                                                                                                                                 Score 10; DB 1; Length 7; Pred. No. 1.4e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.3%; Score 9; DB 1; Length 5; larity 66.7%; Pred. No. 1.48+05; Conservative 0; Mismatches 1; Indele
                                                                                     AMIDATION.
7362D5B69B132310 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION OF THE STANDARD; PRT; 7 AA. P20104; PT; 7 AA. 01-FEB-1991 (Rel. 17, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 01-FEB-1991 (Rel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AA.
FEBS Lett. 323:104-108(1993).
PIR; S33244; S33244.
Neuropeptide; Amidation.
MOD RES
SEQUENCE 7 AA; 965 MW; 73
                                                                                                                                                                 h 30.3%;
Similarity 66.7%;
2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Local 2; Conserve
                                                                                                                                                                 Query Match
Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
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RESULT 8 CCF1\_ENTFA

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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicòtyledons, core eudicots, asterids,
campanulids, Apiales, Apiaceae, Apioideae, Scandiceae, Daucinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phytosulfokine-alpha (PSK-alpha) (Contains: Phytosulfokine-beta (PSK-
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.

MEDLINE=20212743; PubMed=10750705;
Hanai H., Mattern T., Yanamoto M., Matsubayashi Y., Kobayashi T.,
Hanai H., Askapami Y.,
Ramada H., Sakapami Y.,
"A secreted peptide growth factor, phytosulfokine, acting as a stimulatory factor of carrot somatic embryo formation.";

Plant Cell Physiol. 41:27-32(4000).

-!- FUNCTION: In presence of 2.4-D, stimulates proliferation of the cells, but does not stimulate differentiation into the somatic
                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
                                                                                                                                                                                                                                                                                                       Carcinustatin 14.

Carcinus maenas (Common shore crab) (Green crab).

Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca;

Eumalacostraca, Eucarida; Decapoda, Pleocyemata; Brachyura,

Eubrachyura, Portunoidea; Portunidae; Carcinus.
                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
27.3%; Score 9; DB 1; Length 7; 100.0%; Pred. No. 1.46+05; iive 0; Mismatches 0; Indeli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Cerebral ganglion, and Thoracic ganglion; MEDLINE-98121193; PubMed-9461295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
24.2%; Score 8; DB 1; Le
Local Similarity 66.7%; Pred. No. 1.4e+05;
es 2; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S AA.
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Query Match
Best Local Similarity 100.0
Matches 2; Conservative
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                                                                                                                                                                                                              STANDARD;
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                                                                             4 EI 5
                                                                                                                  3 EI 4
                                                                                                                                                                                                            AL14 CARMA
P81817;
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P58261;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                        RESULT 13
AL14 CARMA
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PSK_DAUCA
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Appl. Environ. Microbiol. 58:1417-1422(1992).
-1- PUNCTION: Lanthhonine-containing peptide antibiotic (lantibiotic).
Active on Gram-positive bacteria.
Antibiotic; Bacteriocin; Lantibiotic.
Secure 7 AA; 786 MW; 741776D05B05B810 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Purification and characterization of a new bacteriocin isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1998) to Swiss-Prot.
-!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP
cyclohydrolase I. This inhibition is reversed by L-phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                           Gaps
                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
Cowthorne M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carnobacterium sp. (strain U149).
Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.3%; Score 9; DB 1; Length 7; 75.0%; Pred. No. 1.46+05; tive 0; Mismatches 1; Indels
Query Match 27.3%; Score 9; DB 1; Length 7; Best Local Similarity 66.7%; Pred, No. 1.4e+05; Matches 2; Conservative 0; Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AA; 806 MW; 71B5B057273B4700 CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Lantibiotic carnocin UI49 (Fragment).
                                                                                                                                                                                                                7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (By similarity).
-!- SUBUNIT: Homodimer (By similarity).
SWISS-2DPAGE; P99025; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92321768; PubMed=1622206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Conservative
                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=35782;
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TISSUE=Coleoptile;
TISSUE=Coleoptile;
TOuzet P., Ricardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
Pernollet Word dimensional gel protein database: towards an integrated genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-!-MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.1, its M is: 30.4 kDa.
Maize-2DPAGE; P80628; COLEOPTILE.
                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
-!- SUBCELLULAR LOCATION: Secreted.
-!- PTW: Sulfation is important for activity and for the binding to putative membrane receptor (By similarity).
-!- SIMILARITY: Belongs to the phytosulfokine family.
Growth factor; Sulfation.
1 4 PHYTOSULFOKINE-BETA.
MOD RES 1 SULFATION.
MOD_RES 3 SULFATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment).
Zea mays (Maize).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida; Poales; Poaceae;
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
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        PHYTOSULFOKINE-BZTA.

        MOD_RES
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        SULFATION.

        MOD_RES
        3
        SULFATION.

        SEQÜENCE
        5 AA; 687 MM; 76C1BBS04B300000 CRC64;

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Best Local Similarity 50.v.
1; Conservative
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P80628;
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UC22_MAIZE
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ilarity 50.0%;
Conservative
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Best Local Similarity
2, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
STRAIN=DSM 20451;
PubMed=12112860;
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P82181 spinacia ol
P82182 spinacia ol
Q72100 ceenothabdi
007354 synechococo
P83233 lycopersico
Q85981 human immun
P70804 azotobacter
Q15903 homo appien
Q9yve3 human adeno
Q9yy19 human adeno
Q9y10 human adeno
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Gaps Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
"High pressure effects step-wise altered protein expression in
Lactobacillus sanfranciscensis.";
Proteomics 2:765-774 (2002).
-i- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN ; 0 P83530; 01-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Unknown protein from 2D-page (Fragment). Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco). Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; NCBL TaxID=1625; Score 14; DB 2; Length 7; Pred. No. 1e+06; 0; Indels 2; Mismatches 0; Indels 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;

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6 AA; 675 MW; 6321B415B05DB000 CRC64;
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Best Local Similarity
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nes 3; Conserv
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SEQUENCE FROM N.A.
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Q7Z1C0;
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MEDLINE=20455799; PubMed=10874046;

MEDLINE=20455799; PubMed=10874046;

Amediuchi K., Subramanian A.R.;

The plastid ribosomal proteins. Identification of all the proteins in the plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";

L. Sibol. Chem. 275:28466-28482(2000).

C. SUBLIANCION; THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

C. SUBCLIANCION; THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

C. SUBCLIANCION; THIS PROTEIN BINDS DIRECTLY TO SSUES.

C. TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.

C. TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.

C. SIMILARITY: BELONGS TO THE LIDP FAMILY OF RIBOSOMAL PROTEINS.

GO; GO:0019843; F:RRNA binding; IEA.

GO; GO:001843; F:RRNA binding; IEA.

GO; GO:001843; F:RRNA binding; IEA.

RO; GO:00186507; C:chloroplast; IRAA.

RO; GO:00186507; C:chloroplast; IRAA.

ROSIES; PSOII09; RIBOSOMAL LIO, PARTIAL.

RIBOSOMAL LIO, PARTIAL.

RIBOSOMAL LOSIES; ROSIES; ROSIES; RON TER

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SEQÜENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;
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MEDLINE=20435798; PubMed=10874046;

Wamaguchi K., Subramanian A.R.;

"The plastid ribosomal proceins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";

"The Diastid ribosomal proceins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";

"The Chem. 275:28466-28482(2000).

"I BIOL Chem. 275:28466-28482(2000).

"I FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

"I FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

"I FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

"I FISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.

"I TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.

"I SIMILARITY: BELONGS TO THE LIOP FAMILY OF RIBOSOMAL PROTEINS.

GO; GO:0019843; F:TRNA binding; IEA.

GO; GO:0019843; F:STRNA binding; IEA.

GO; GO:0003735; F:Structural constituent of ribosome; IEA.

RIBOSOMAL LIO; PARTIAL.

"W Ribosomal protein; Chloroplast; rRNA-binding.

"W Ribosomal protein; Chloroplast; rRNA-binding.
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01-JUN-2000 (TEMBLrel. 14, Created)
01-JUN-2000 (TEMBLrel. 14, Last sequence update)
01-OCT-2003 (TEMBLrel. 15, Last annotation update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
Chloroplast 50S ribosomal protein LIO beta (Fragment).
Spinacia oleracea (Spinach).
Spinacia oleracea (Spinach).
Spermatophyta; Viidiplantee; Streptophyta; Embryophyta; Tracheophyta;
Caryophylales; Amaranthaceae; Spinacia.
ONCBL TaxID=3562;
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 15, Last annotation update)
Chloroplast 50s ribosomal protein L10 gamma (Fragment).
Spinacia oleracea (Spinach).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophylales; Amaranthaceae; Spinacia.
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39.4%; Score 13; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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Bacteria: Cyanobacteria; Chroococcales; Cyanothece.
NCBL_TaxID=41431;
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Length 6;
                                            Indels
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.larity 66.7%; Pred. No. 1e+06;
Conservative 1; Mismatches 0; Indels
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STRAIN=Bristol N2;
Bradshaw H., Graves T., Blair T.;
"The second of Celegans cosmid Wolbl1.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF043704; AA038592.1; -.
Hypothetical protein.
SEQUENCE 7 AA; 874 MW; 72D1A9DB5041A6F0 CRC64;
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DB 10;
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39.4%; Score 13; 100.0%; Pred. No.
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MEDLINE=99069613; PubMed=9851916;
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01-0CT-2003 (TrEMBLrel. 25, Las
01-0CT-2003 (TrEMBLrel. 25, Las
Hypothetical protein W01B11.6.
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01-JUL-1997 (TrEMBLrel. 04,
01-JUL-1997 (TrEMBLrel. 04,
01-DEC-2001 (TrEMBLrel. 19,
                                            Conservative
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MEDLINE=22056123; PubMed=12060770; MEDLINE=22056123; PubMed=12060770; MeDLINE=22056123; PubMed=12060770; Hoffmann D., Korn K., Selbig J.; Molter H., Kaiser R., Lengauer T., Moffmann D., Korn K., Selbig J.; "Diversity and complexity of HIV-1 drug resistance: A bioinformatics approach to predicting phenotype from genotype."; Proc. Natl. Acad. Sci. U. S.A. 99:8271-8276(2002).
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Rehm B.H.A., Exteswag H., Valla S.;
"A new Azotobacter vinelandii mannironan C-5-epimerase gene (algG) is
part of an alg gene cluster physically organized in a manner similar
to that in Pseudomonas aeruginosa.";
J. Bacteriol. 178:5884-5889 (1996).
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SEQUENCE FROM N.A.
TISSUB=Placenta;
Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pseudomonadaceae; Azotobacter.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last and
(Clone XP7878) (Fragment).
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     [1]
SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huang T.C., Lin R.F., Chu M.K., Chen H.M.; "Organization and expression of nitrogen-fixation genes in the aerobic nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum (Tomato).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; asterids;
Ismiids; Solanales; Solamaceae, Solanum.
                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                             Query Match 27.3%; Score 9; DB 2; Length 7; Best Local Similarity 66.7%; Pred. No. 1e+06; Matches 2; Conservative 0; Mismatches 1; Indels
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (BC 4.4.1.14)
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1-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Truncated pol protein (Fragment).
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBL_TaxID=11676,
                                                                                                                                                                                                                                                   7 AA; 849 MW; 7412C72AA9D5B030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AA; 828 MW; 71B412C7377415D0 CRC64;
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                                                                 MEDLINE=99231861; PubMed=10217509;
                                                                                                                                                                            Microbiology 145:743-753(1999).
EMBL, AF003700; AAC35193.1; -.
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                      SEQUENCE FROM N.A.
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P93233
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SEQUENCE FROM N.A.
MEDINE-99039045; PubMed-9882155;
Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,
Enjuanes L.;
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                                                                                                                                                                                                                                0; Gaps
"Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
Submitted (WAY-1998) to the EMBL/GenBank/DDBJ databases.
BMBL; AR065064; AAD03659.1; -.
EMBL; AR065062; AAD03659.1; -.
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MEDLIA:e86079100; PubMed=2825919;
MEDLIA:e86079100; PubMed=2825919;
Rasiofnae:e807910; Jaude H.;
Rasiofnae:e Coronavirus TGEV: partial sequence of the genomic RNA its organization and expression.";
Biochimie 69-591-600(1987).
Biochimie 69-591-600(1987).
SEQUENCE 7 AA, 927 NW; 69050727335726F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmissible gastronteritis virus.
Viruses, SBRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Replication and packaging of transmissible gastroenteritis coronavirus-derived synthetic minigenomes."; J. Virol. 73:1535-1545(1999).
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Conservative 2; Mismatches 1; Indels
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24.2%; Score 8; DB 12; Length 7;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 1; Conservative 1; Mismatches 1; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
01-OCT-2001 (Fragment).
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 19, Last annotation update)
Hypothetical fusion protein,
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es 1; Conserv
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O9YIRO;
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Q9YIRO
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                Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human adenovirus type 7.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
VCBI_TaxID=10519;
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Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
"Strain variation in adenovirus serotypes 4 and 7a causing acute
                                   Caskey C.T.H.;
"Isolation of chromosome-specific genes by reciprocal probing of
"Isolation of chromosome specific genes by reciprocal probing of
arrayed conA. Mol. Genet. 0:0-0(1995).
Hum. Mol. Genet. 0:0-0(1995).
EMBL: L32082; AAA73893.1; -.
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Crawford-Mikeza L.K.;
Submitred (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065065; AAD03662.1;
NON_TER
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAY-1999 (TrEMBLrel. 18, Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PVI core protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      piratory disease.";
Clin. Microbiol. 37:1107-1112(1999).
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09Y1Q9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                  Gaps
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                                                  SEQUENCE FROM N.A.
STRAID=KN T96-0620, S-1058, and CL 68578;
Crawford-Mikeza L.K., Nang R.N., Schnurr D.P.;
Crawford-Mikeza L.K., Nang R.N., Schnurr D.P.;
Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
Submitteed (Max-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF065068; AAD03668.1;
EMBL, AF065066; AAD03668.1;
EMBL, AF065067; AAD03666.1;
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01-JUN-2003 (TERMELTE1. 24, Last sequence update)
01-JUN-2003 (TERMELTE1. 24, Last sequence update)
01-JUN-2003 (TERMELTE1. 24, Last annotation update)
Pheromone peptide ILME.
Sepia officinalis (Common cuttlefish).
Bekaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
NCBI_TAXID=6610;
Human adenovirus type 7a.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
Vopi_TaxID=85755;
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"Cloning and sequencing of 3' UTR of EXFABP gene in chicken.",
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AF487519; AAL96665.1; -.
NON TER 1
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1e+06;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Extracellular fatty acid binding protein (Fragment).
                                                                                                                                                                             SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;
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Pred. No. 1e+0
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Best Local Similarity
Matches 1; Conserv
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TISSUE=Blood;
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SPECTROMETRY
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RC TISSTE=Egg;

RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;

RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;

RT officinalis.";

RI Biochem. Biophys. Res. Commun. 275:217-222(2000).

RY SEQUENCE.

RC TISSUE=Egg;

RX PubMed=12207899;

RX PubMed=12207899;

RY TISSUE=Egg;

RY TISSUE=Egg;

RY PErtilization in Sepia officinalis: the first mollusk sperm-
RT TRACTING COMMUN. 296:1186-1193(2002).

RY TISSUE SPECIFICITY: FOLICIE. FULLY GROWN OCCYTE AND EGG(EC2).

CC -1- FUNCTION: HAS WYORROPIC ACTIVITY TARGETING THE GENITAL TRACT.

CC -1- FUNCTION: HAS SPECIFICITY: FOLICIE. FULLY GROWN OCCYTE AND EGG(EC2).

CC -1- TISSUE SPECIFICITY: FOLICIE. FULLY GROWN OCCYTE AND EGG(EC2).

CC -1- TISSUE SPECIFICITY: FOLICIE. FULLY GROWN OCCYTE AND EGG(EC2).

CC -1- TISSUE SPECIFICITY: FOLICIE. FULLY GROWN OCCYTE AND EGG(EC2).

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CC -1- TISSUE SPECIFICITY: FULLY GROWN OCCYTE AND EGG(EC2).

CC -1- TISSUE SPECIFICITY: FULLY GROWN OCC
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - protein search, using sw model	n: June 2, 2004, 18:47:08; Search time 49 Seconds (without alignments) 40.364 Million cell updates/sec	: US-09-712-819D-12 ct score: 33 nce: 1 FTLEISR 7	ng table: BLOSUM62 Gapop 10.0 , Gapext 0.5	hed: 1586107 segs, 282547505 residues	Total number of hits satisfying chosen parameters. 92273
	OM protein -	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

seq length: seq length:

Minimum DB & Maximum DB &

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\* A\_Geneseq\_29Jan04:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Vascular DPI trypt Schizophr Depressio Schizophr Human API Multiple Prostate Prostate Breast ca Breast ca Alzheimer Alzheimer 84 derive S4 deriva Scaffold Scaffold Staphyloc Staphyloc Staphyloc Human afa Rheumatoi Vascular Vascular deriva Aay41889 R Abb55870 v Abb56283 v Abb55981 v Aau28602 D Aau24969 S Aau26249 | Aau15313 & Aau15313 & Aau15313 & Abb52150 & Abb52155 & Abg78730 & Abg58010 & Abb57255 & Abb57203 & Abr59010 & Aab30076 Abr45678 Abr46070 Aar81848 Aay40736 Aay40738 SUMMARIES ABP58010 ABP57255 ABP57203 ABB55981 AAU28602 ABB52355 ABG78901 ABR59010 ABR59042 ABR46070 AAB30074 Length Query Result No. 

Abr44950 Staphyloc Abr45462 Staphyloc Abr45542 Staphyloc Aar07556 Ribonucle Aay42013 Rheumatoi Aaw82668 Cauliflow	ഗയഗയാ	304107	Aay83858 Ribonucle Aab30075 Scaffold Aab47357 Cell 1ysi Adb79629 Parapoxvi Aaw84431 HIV-1 nuc
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26 23 33 31		2 K K K K K K K K K K K K K K K K K K K	4 4 4 4 4 1 5 6 4 5

## ALIGNMENTS

Human, afamin, serum protein family, albumin, alpha-foetoprotein, plasma, vitamin D binding protein, homology, post-translational processing, teromatography, Primer, Prim, amplification, probe, rheumatoid arthritis, ischaemia-reperfusion injury, ARDS, cardiopulmonary bypass, sepsis, toxic plasma substance; inflammation. Human afamin tryptic fragment FX20. Æ 94US-00222619 95WO-US004075 AAR81848 standard; peptide; (AMGE-) AMGEN INC. (UYRQ ) UNIV ROCKEFELLER (first WO9527059-A1. Homo sapiens 31-MAR-1995; 31-MAR-1994; 16-MAY-1996 12-0CT-1995 AAR81848; RESULT 1 AAR81848 

Wright Wurfel MM, Lichenstein HS, Lyons DE, WPI; 1995-358634/46 Human afamin or a variant and poly:nucleotide(s) encoding it - a human serum protein with activities in common with other members of this

Example 3; Page 45; 97pp; English.

family

Peptides AAR81847-54 are tryptic peptide fragments from human afamin (AAR81845) novel member of the human serum protein family. The fragments were used to design primers and probes (AAT00786-98) for the cloning of the afamin gene (AAT00785) from human liver cDNA. Afamin is thought to have similar properties to human albumin, alpha-foetoprotein and vitamin b binding protein due to homology with these proteins. The gene encodes a mature protein of 66576 daltons without post-translational processing (ca. 87000 daltons with post-translational processing isolated from human plasma by a conventional chromatographic methods. The

Abr46854

ABR46854

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dimensional array of features. The method can be used for screening, dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a method can be used for screening, of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally sources; (a) analysing a sample of serum or plasma and optionally symbol by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature of features in the sample indicates the presence or absence of serum or plasma from the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic protein isoforms (RPIs), and for production of antibodies to RPIs. The RA-diagnostic feature (RAPIs) proceins can be used to identify compounds that promote or inhibit their activity, which are then used as proceouls. AAV41844 to AAV42101 represent RA propocoles contains RAPS can be used in gene therapy proceouls. AAV41844 to AAV42101 represent RPI peptidies, AAV442101 represent SPIS, which are all AAV42101 represent proceed process and
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protein can be used to ameliorate ischaemia-reperfusion injury, rheumatoid arthritis, ARDS, cardiopulmonary bypass, sepsis, toxic plasma substances released after inflammation, etc
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection; rheumatoid arthritis diagnostic feature; RRPI; synovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A method has been developed for the diagnosis of human rheumatoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosis of human rheumatoid arthritis by two-dimensional
                                                                                                                       72.7%; Score 24; DB 2; Length 7; 71.4%; Pred. No. 1.4e+06; 1ve 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 18; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Townsend RR;
                                                                                                                                                                                                                                                                                                                                                         AAY41889 standard; peptide; 7 AA.
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                                                                                                  Query Match
Best Local Similarity 71...
5, Conservative
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                                                                                    Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
                                                                                                                                                                                                                                                                                                                                                                                                                     Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
                                                                                                           Gaps
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Pred. No. 1.48+06;
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                                                                                                                                                                                                                                                                                                                                                                                  Vascular dementia-associated protein isoform (VPI) 70.
used in the exemplification of the present invention
                                                                                                         2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis; prognosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herath HMAC, Parekh RB, Rohlff C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 31; 151pp; English.
                                                                                                                                                                                                                                                                        ABB55870 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-2000; 2000GB-00006285.
24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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                                                                   h 72.7%;
Similarity 57.1%;
4; Conservative
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                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                             1 FTLEISR 7
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                                   Sequence 7 AA;
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Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;

diagnosis; prognosis; gene therapy.

WO200169261-A2.

20-SEP-2001.

Homo sapiens.

Vascular dementia-associated protein isoform (VPI) 181

15-FEB-2002 (first entry)

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Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
                                                                                                                                           VD; VD-associated protein isoform; VPI; screening;
                                                                                                                        Vascular dementia-associated protein isoform (VPI) 483,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of VD and for gene therapy
                                                                                                                                                                                                                                                                                               (OXFO-) OXFORD GLYCOSCIENCES UK LID.
                                                                                                                                                      diagnosis; prognosis; gene therapy.
                                                                                                                                                                                                                                                                                                                   Rohlff C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.7%; Scor.
57.1%; Pred
2; 1
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                                                           ABB56283 standard; peptide; 7 AA
                                                                                                                                                                                                                                                       15-MAR-2000; 2000GB-0006285.
24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
                                                                                                                                                                                                                                    14-MAR-2001; 2001WO-GB001106.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                          Vascular Dementia;
1 YTFELSE
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YTFELSE
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                                                                                                   15-FEB-2002
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                                                                                ABB56283;
                                                  ABB56283
                                         RESULT
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Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.

Claim 6; Page 33; 151pp; English.

(OXFO-) OXFORD GLYCOSCIENCES UK LTD.

15-MAR-2000; 2000GB-00006285. 24-NOV-2000; 2000GB-00028734. 28-NOV-2000; 2000US-00724391. 14-MAR-2001; 2001WO-GB001106

Rohlff C;

Parekh RB,

Herath HMAC,

WPI; 2001-557937/62

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Sequence 7 AA;
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AAU28602
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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABBS501-ABBS6295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the serenting of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids a constaint of VD, in inhibiting the function of a VPI are useful for the
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Pred. No. 1.4e+06;
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ABB55981 standard; peptide; 7 AA.

RESULT 5
ABB55981
ID ABB5
XX
AC ABB5

ABB55981;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSP) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABB55801-ABB56595) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
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DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
maniac-depressive illness; schizoaffective disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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Pred. No. 1.4e+06;
2; Mismatches 1;
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Best Local Similarity
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Preparation for diagnosing or treating bipolar affected disorder (BAD) or unipolar depression, or for screening for modulators, comprises a BAD-associated protein isoform.
                                                                                                                                                                                                                                          New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs
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                                                                                                                     Tyson KL.
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                                                                                                                        Terrett JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Depression-Associated Protein isoform DPI-208.
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                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 32; 148pp; English.
                                                          (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                        Rohlff C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim B; Page 34; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU26249 standard; peptide; 7 AA.
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08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
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57.18;
28-DEC-2000; 2000US-00750395
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Best Local Similarity
Matches 4; Conserv
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The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest deptides of these proteins. Some of the DPIs (AMU28404-AMU2842) beptides of these proteins. Some of the DPIS (AMU28404-AMU2843) at affective disorder) ambjects, whilst other DPIs (AMU28626-AMU28837) are increased in BAD subjects. Also described are peptide sequences increased in BAD subjects. Also described are peptide sequences can oppressed by The sequences of the invention are useful for clinical screening, diagnosis, prognosis, therapy and prophylaxis of neuropsychatric disorders e.g. BAD (also known as bipolar mood disorder, schizoaffective disorders, attention deficit disorders, schizoaffective disorders, attention deficit disorders. The present sequence represents one of the DPI tryptic digest peptides of the present

Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.

Disclosure, Page 34; 153pp; English.

Tyson KL;

Terrett JA,

Rohlff C,

Parekh RB,

Herath HMAC,

WPI; 2001-570626/64.

OXFO-) OXFORD GLYCOSCIENCES UK LTD

24-FEB-2000; 2000GB-00004412. 08-DEC-2000; 2000GB-00030050. 12-DEC-2000; 2000US-0254830P.

23-FEB-2001; 2001WO-GB000786.

WO200162787-A1

30-AUG-2001.

Homo sapiens

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Gaps . 0

1; Indels Length 7;

Score 24; DB 4; I Pred. No. 1.4e+06; 2; Mismatches 1.

72.7%;

4; Conservative

Matches

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Query Match Best Local Similarity

Seguence 7 AA;

Schizophrenia-associated protein isoform, SPI, SPI-206, SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.

24-FEB-2000; 2000GB-00004415.

23-FEB-2001; 2001WO-GB000792

WO200162785-A2

30-AUG-2001

Homo sapiens

Schizophrenia-Associated Protein Isoform (SPI) peptide #198.

18-DEC-2001 (first entry)

AAU24969;

AAU24969 standard; peptide; 7 AA.

RESULT 7 AAU24969

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The invention relates to a preparation comprising an isolated Bipolar Associated Protein Isoform (DPIS). The DPI's are used to screen, diagnose or prognose of BAD or unipolar depression, dentify a ceremine the stage or severity of BAD or unipolar depression, dentify a cheer is so is developing BAD or unipolar depression, or monitor the subject at risk of developing BAD or unipolar depression, or monitor the cleentify agents that interact with a DPI. These agents, antibodies daying the DPIS, and mucleic acids encoding the DPIS are used to treat a capinate the DPIS, and mucleic acids encoding the DPIS are used to treat a capinate the DPIS, and mucleic acids encoding the DPIS are used to treat a capinate the disorder. A schizoaffective disorder, a bipolar or a creening approach of using DPIS for screening, diagnosis of BAD or unipolar depression overcomes the problems of using gene expression analysis, such as not being able to obtain central nervous present sequence is a DIP decreased in the CSF (cerebro-spinal fluid) of subjects having BAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing and monitoring Schizophrenia by detecting the presence of Schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid.
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                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 4; Length 7; Pred. No. 1.4e+06; 2; Mismatches 1; Indels
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57.18;
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28-DEC-2000; 2000US-00750395
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Best Local Similarity
Matches 4; Conserv
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1 YTFELSR 7
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SCH and the relative abundance of at least 1 chosen feature correlates with the presence or absence of SCH; and (2) monitoring the effect of therapy administered to a subject with SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The expression and activity of the SFS, SPIs and related molecules (e.g. secondary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectiveness of treatment and a targets to identify and produce potential therapeutic agents for the treatment of SCH. The paucity of detectable neuralgic defects distinguishes neuropsychiatric disorders such as SCH from neurological disorders, where manifestations of anatomical and biochemical changes have been identified in many cases. Consequently the identification and characterisation of cellular and/or molecular causative defects and neuropathies are measured to improve treatment of neuropsychiatric disorders. AAUISI14-AAUIS762 represent the amino acid sequences of schizophrenia-associated isoforms used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for Alzheimer's disease in a mammal, by making two-dimensional array of a feature whose relative abundance correlates with disease, and comparing with abundance of the feature in samples of healthy persons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to methods for the screening, diagnosis and prognosis of Alzheimer's disease. The methods involve the detection of Alzheimer's Disease-Associated Features (AFE) and Alzheimer's Disease-Associated Features (AFE) and Alzheimer's Disease-Associated Protein Isoforms (APIS) in cerebrospinal fluid, serum or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; neuroprotective; nootropic; gene therapy; vaccine;
Alzhedimer's disease; Alzhedimer's Disease-Associated Feature;
Alzheimer's Disease-Associated Protein Isoform; API; tryptic
Expression Reference Protein Isoform; ERPI; proteolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                      72.7%; Score 24; DB 4; Length 7; 57.1%; Pred. No. 1.4e+06;
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28-NOV-2000; 2000US-0253647P
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7 AA;
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Matches
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Pred. No. 1.4e+06; 2; Mismatches 1

Similarity 57.1 4; Conservative

Best Local Matches

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The invention relates to methods for the screening, diagnosis and prognosis of Alzheimer's disease. The methods involve the detection of Alzheimer's Disease-Associated Features (AFS) and Alzheimer's Disease-Associated Features (AFS) and Alzheimer's Disease-Associated Protein Isoforms (AFS and APIS) in cerebrospinal fluid, serum or Expression Reference Protein Isoform (ERPI) in order to determine whether a patient is suffering from, or has a predisposition to, Alzheimer's Disease. The relative abundance of the AFS and APIS correlates with the severity of Alzheimer's Disease. The present sequence is a peptide produced from an API by proteolysis
plasma. The abundance of the AFs and APIs is then normalised to an Expression Reference Protein Isoform (ERPI) in order to determine whether a patient is suffering from, or has a predisposition to, Alzhahmer's Disease. The relative abundance of the AFs and APIs correlates with the severity of Alzhaimer's Disease. The present sequence is a peptide produced from an API by proteolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for Alzheimer's disease in a mammal, by making two-dimensional array of a feature whose relative abundance correlates with disease, and comparing with abundance of the feature in samples of healthy persons.
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; neuroprotective; nootropic; gene therapy; vaccine;
Alzhaimer's disease; Alzhaimer's Disease-Associated Feature; AF;
Alzheimer's Disease-Associated Protein Isoform; AFI; tryptic digest;
Expression Reference Protein Isoform; ERPI; proteolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Durham KL, Friedman DL, Herath HVAC, Kimmel LH, Parekh RB;
Potter DM, Rohlff C, Silber BM, Stiger TR, Sunderland PT;
Townsend RR, White F, Williams SA;
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                                                                                                                                                              72.7%; Score 24; DB 4; Length 7; 71.4%; Pred. No. 1.4e+06; Live 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                        ABB52355 standard; peptide; 7 AA
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                                                                                                                                 Sequence 7 AA;
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ABB52355
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This invention relates to a novel method for screening or diagnosing consisting multiple sclerosis (MS) in a subject to determine the stage or severity conf. MS. to identify a subject at risk of developing MS or to omnitor the effect of a therapy administered. The method comprises analysing a sample confect of a therapy administered. The method comprises analysing a sample conficing the presence of multiple sclerosis-associated features (MSFS), detecting the presence of multiple sclerosis-associated features (MSFS), of the invention correspond to spots identified on a 2D gel these proteins the invention correspond to spots identified on a 2D gel these proteins convention and the compositions are useful for clinical screening.

Confidence may have antiinflammatory or neuroprotective activity. The methods of the invention and treatment of MS, for monitoring the effectiveness of MS treatment. For selecting participants, in clinical trials, for identifying the respond to a particular therapeutic treatment and constitution or delay to expression or activity of an MSPI are useful for treatment and MS, to prevent or delay the progression or activity of an MSPI are useful for preventing or delaying the onset or development of MS, to prevent or delay the progression of MS, or to ameliorate the symptoms MS. Nucleic confidence the fragments are useful for promoting number of therapy. The present sequence represents a human multiple sclerosis therapy. The present sequence represents a human multiple sclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening or diagnosing multiple sclerosis (MS), useful for e.g. determining the stage or severity of MS, comprises detecting the presence of MS-associated features or protein isoforms by 2-dimensional
                                                                                                                                                                                                                                                         Multiple sclerosis associated feature (MSF) tryptic digest peptide #389.
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                                                                                                                                                                                                                                                                                                Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF; human; multiple sclerosis-associated protein isoform; MSPI; antiinflammatory; neuroprotective.
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                                                                                                                                       ABG78901 standard; peptide; 7 AA.
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20-NOV-2001; 2001US-0331647P.
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                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herath HMAC, Parekh RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-599812/64.
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1 YTFELSR
1 FTLEISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        electrophoresis
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                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200259604-A2
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                          29-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-2002.
                                                                                                                                                                                   ABG78901;
                                                                                                    RESULT 12
                                                                                                                          ABG78901
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7

Length

DB 4;

72.7%; Score 24;

7 AA;

Sequence Query Match ABP58010 standard; peptide; 7 AA

RESULT 14

ABP58010

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This invention relates to a novel method for screening or diagnosing multiple sclerosis (MS) in a subject to determine the stage or severity of MS, to identify a subject at risk of developing MS or to monitor the effect of a therapy administered. The method comprises analysing a sample body fluid from the subject by two-dimensional electrophoresis and detecting the presence of multiple sclerosis-associated features (MSFB), or multiple sclerosis-associated protein isoforms (MSFB). The MSF's of the invention correspond to special identified on a 2D gel these proteins may have antinflammatory or neuroprotective activity. The methods of the invention and the compositions are useful for clinical screening, diagnosis and treatment of MS, for monitoring the effectiveness of MS treatment, for selecting participants in clinical trials, for identifying participants in clinical trials, for identifying teatients most likely to respond to a particular therapeutic treatment and for screening and developing drugs for treatment of MS. Agents that modulate the expression or activity of an MSPI are useful for treating or delaying the onest or development of MS. Nucleic acids comprising a sequence encoding an MSPI, MSPI function by gene therapy. The present sequence represents a human multiple sclerosis associated feature tryptic digest peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening or diagnosing multiple sclerosis (MS), useful for e.g. determining the stage or severity of MS, comprises detecting the presence of MS-associated features or protein isoforms by 2-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multiple sclerosis associated feature (MSF) tryptic digest peptide #218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF; human; multiple sclerosis-associated protein isoform; MSPI; antiinflammatory; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.7%; Score 24; DB 5; Length 7; Best Local Similarity 57.1%; Pred. No. 1.4e+06; Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 26, 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herath HMAC, Parekh RB, Rohlff C;
                                                                                                                                                                                                                                                                         ABG78730 standard; peptide; 7 AA.
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20-NOV-2001; 2001US-0331647P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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1 FTLEISR
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1 YTFELSR
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The present sequence is that of a peptide fragment of a novel human 50.8 kDa prostate cancer-associated protein that has been identified as a high prostate cancer. The novel protein includes a polypeptide that is related to human serum vitamin D binding protein includes a polypeptide that is related to human serum vitamin D binding protein (VDBP, see ABPS8017). The present peptide corresponds to amino acids 146-150 that distinguish VDBP-related broteins of peptides (see ABPS8005-16) that distinguish VDBP-related proteins of proteins, or which may be characterised as binding specifically to an anti-VDBP antibody. VDBP-related proteins are detectable at a higher concentration in serum from a mammal, e.g. a human, with prostate cancer relative to serum from a healthy mammal and can therefore be used as proteate cancer markers. They permit the rapid detection, preferably before metastases occur, of prostate cancer. A target profetae cancer-associated protein may be detected using a labelled antibody capable of binding specifically to the prostate cancer also useful as targets for treating prostate cancer, and as indicators for monitoring the efficiency of prostate cancer, therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing or treating prostrate cancer by detecting in a sample isolated from the individual the presence of prostate cancer-associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                                                                                                             Prostate cancer; marker; vitamin D binding protein; VDBP; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.7%; Score 24; DB 6; Length 7; 57.1%; Pred. No. 1.46+06; ive 2; Mismatches 1; Indels
                                                                                             Prostate cancer marker protein peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP57255 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 41; 63pp; English.
                                                                                                                                                                                                                                                                                                                                       30-NOV-2000; 2000US-0250284P.
                                                                                                                                                                                                                                                                                                     30-NOV-2001; 2001WO-US045031,
                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hlavaty J, Briggman JV;
                                                                                                                                                 diagnosis; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                 (MATR-) MATRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-067369/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FTLEISR 7
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                                                                                                                                                                                         Homo gapiens.
                                                       11-FEB-2003
                                                                                                                                                                                                                                                               26-SEP-2002
                   ABP58010;
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ID ABP5
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AC ABP5
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ABP57255;

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Gaps

Search completed: June 2, 2004, 18:57:50 Job time: 51 secs

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16-APR-2003 (first entry)
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Breast cancer associated tryptic digest peptide SEQ ID NO:154.

Breast cancer associated feature, BF; BPI; breast cancer; diagnosis; breast cancer associated protein isoform; cytostatic; gene therapy.

Synthetic.

WO200288750-A2.

07~NOV-2002;

02-MAY-2002; 2002WO-GB002022.

02-MAY-2001; 2001GB-00010790.

27-JUL-2001; 2001GB-00018385. 14-NJG-2001; 2001GB-00019791. 14-AJG-2001; 2001GB-00028045. 22-NOV-2001; 2001GB-00028065.

(OXFO-) OXFORD GLYCOSCIENCES UK LTD.

Herath HMAC;

WPI; 2003-175048/17.

Screening, diagnosing or determining the stage or severity of breast cancer, composites analyzing and quantitatively detecting Breast Cancer-Associated Peatures or Breast Cancer-Associated Protein Isoforms in a biological sample.

Example, Page 77; 88pp; English.

The present invention describes a method for screening, diagnosing or determining the stage or severity of breast cancer, identifying a subject at risk of developing breast cancer, by generating a two-at risk of developing breast cancer, by generating a two-diministered to a subject with breast cancer, by generating a two-diministered to a subject with breast cancer, by generating a two-diministered to a subject with breast cancer, by generating a two-diministered to a subject with breast cancer, by generating a two-diministered (BPIs). Also described: (1) an antibody capable of immunospecifically binding to one of the BPIs; (2) a pharmaceutical compositions comprising: (4) a BPI, or a nucleic acid encoding a BPI, and a carrier; (3) screening for agents that interact with one compositions comprising: (4) screening for agents that interact with one or more BPIs, BPI fragments, polypeptides related to BPIs, or BPI-fusion proteins; (4) screening for or identifying agents that modulate the composition or activity of one or more BPIs, a BPI related polypeptide, or BPI-fusion proteins; and (5) treating or preventing the present invention can be used for screening, diagnosing or determining the stage or severity of breast cancer. The antibodies, BPIs, and anchoring breast cancer, identifying a subject at risk of developing breast cancer, in monitoring the effect of therapy or monitoring the Energy administered to a subject with breast cancer. The antibodies, BPIs, nucleic acids encoding the BPIs, or an agent that modulates the activity administered to a subject with breast cancer. The antibodies, BPIs, and concerning the BPIs or an agent that modulates the activity of one or more BPIs are useful for treasting or preventing breast cancer. ABPISTION to 
Sequence 7 AA;

72.7%; Score 24; DB 6; Length 7; 57.1%; Pred, No. 1.4e+06; tive 2; Mismatches 1; Indels Best Local Similarity 57.13 Matches 4; Conservative Query Match

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Sequence 7, Appli Sequence 7, Appli Sequence 31, Appl Sequence 312, Appl Sequence 636, Appl Sequence 637, Appl

Sequence 639, Sequence 651, Sequence 653,

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Sequence 198, Application US/09791378
Patent No. US20020142303A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: SCHIZOPHRENIA
TITLE OF INVENTION: SCHIZOPHRENIA
FILE REPRENCE: 9105-061-999
CURRENT APPLICATION NUMBER: US/09/791,378
CURRENT APPLICATION NUMBER: 09/750,395
PRIOR APPLICATION NUMBER: 09/750,395
PRIOR APPLICATION NUMBER: 09/750,395
NUMBER OF SEQ ID NOS: 677
SOFTWARE: Patentin Version 3.0
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US-09-998-909-7
Sequence 7, Application US/0998909
Patent No. US20020164664A1
GENERAL INFORMATION:
APPLICANT: Havaty, John
APPLICANT: Briggman, Joseph
TITLE OF INVENTION:
TITLE OF INVENTION: Detection and Treatment of Prostate Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 72.7%; Score 24; DB 9; Length 7; Best Local Similarity 57.1%; Pred. No. 1e+06; Matches 4; Conservative 2; Mismatches 1; Indels
                                                  US-10-287-892-7

US-09-10-328-340-7

US-09-10-328-953-42

US-10-367-593-312

US-10-367-594-312

US-10-367-594-312

US-10-367-658-312

US-10-367-658-312

US-10-367-658-312

US-10-368-636

US-10-368-636

US-10-395-032-636

US-10-395-032-636

US-10-395-032-636

US-10-395-032-636

US-10-395-032-637

US-10-06-869-653

US-10-06-869-653

US-10-06-869-653

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US-10-395-032-639

US-10-395-032-639

US-10-395-032-639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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US-09-791-378-198
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    Sequence 198, Appli
Sequence 7, Appli
Sequence 205, App
Sequence 370, App
Sequence 145, App
Sequence 145, App
Sequence 105, App
Sequence 131, App
Sequence 4, Appli
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Sequence 6, Appli
Sequence 39, Appl
Sequence 6, Appli
                                                                                                                          2, 2004, 18:59:52 ; Search time 37.5 Seconds (without alignments) 52.517 Million cell updates/sec
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1: \( \cgn2 = 6 \) ptodata3 \( \) fubba3 \( \) USCOMB.pep:*

2: \( \cgn2 = 6 \) ptodata2 \( \) pubpa3 \( \) USCOMB.pep:*

3: \( \cgn2 = 6 \) ptodata2 \( \) pubpa3 \( \) USCOMB.pep:*

4: \( \cgn2 = 6 \) ptodata2 \( \) pubpa3 \( \) USCOMB.pep:*

5: \( \cgn2 = 6 \) ptodata2 \( \) pubpa3 \( \) USCOMB.pep:*

6: \( \cgn2 = 6 \) ptodata2 \( \) pubpa3 \( \) USCOMB.pep:*

6: \( \cgn2 = 6 \) ptodata3 \( \) pubpa3 \( \) USCOMB.pep:*

7: \( \cgn2 = 6 \) ptodata3 \( \) pubpa3 \( \) USGOMB.pep:*

8: \( \cgn2 = 6 \) ptodata3 \( \) pubpa3 \( \) USGOMB.pep:*

9: \( \cgn2 = 6 \) ptodata3 \( \) pubpa3 \( \) USGOMB.pep:*

10: \( \cgn2 = 6 \) ptodata3 \( \) pubpa3 \( \) USGOB PUBCOMB.pep:*

11: \( \cgn2 = 6 \) ptodata3 \( \) pubpa3 \( \) USGOB PUBCOMB.pep:*

12: \( \cgn2 = 6 \) ptodata3 \( \) pubpa3 \( \) USGOB PUBCOMB.pep:*

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13: \( \cgn2 = 6 \) ptodata3 \( \) pubpa3 \( \) USGOB PUBCOMB.pep:*

14: \( \cgn2 = 6 \) ptodata3 \( \) pubpa3 \( \) USGOB PUBCOMB.pep:*

15: \( \cgn2 = 6 \) ptodata3 \( \) pubpa3 \( \) USGOB PUBCOMB.pep:*

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16: \( \cgn2 = 6 \) ptodata3 \( \) pubpa3 \( \) USGOB PUBCOMB.pep:*

17: \( \cgn2 = 6 \) ptodata3 \( \) pubpa3 \( \) USGOB PUBCOMB.pep:*

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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-988-909-7
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US-10-264-309-146
US-10-264-309-146
US-10-264-309-146
US-10-264-309-146
US-10-264-309-146
US-10-284-309-146
US-10-238-965-4
US-10-238-965-4
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US-10-238-965-4
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US-10-238-965-4
US-10-288-965-4
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Maximum Match 1008
Listing first 45 summaries
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Match Length
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                                                                                                                                                                                                      Title:
Perfect score:
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                                                                                                                                                                                                                                            Sequence:
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                                                                                                                                Run on:
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Gaps

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Friedman, David L.
Herath, Herath Mudiyanselage Athula Chandrasiri
                                                                                                              Potter, David M.
Rohlff, Christian
Silber, B. Michael
Stiger, Thomas R.
Sunderland, P. Trey
Townsend, Robert Reid
White, Frost
                                                                 Kimmel, Lida H.
Parekh, Rajesh Bhikhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: homo sapien
US-09-826-290-370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: homo sapien
US-09-791-393-145
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Best Local Similarity
Matches 4; Conserv
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1 YTFELSR 7
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US-09-791-393-145
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APPLICANT: Friedman, David L.
APPLICANT: Friedman, David L.
APPLICANT: Friedman, David M.
APPLICANT: Knimel, Lida H.
APPLICANT: Rajeah Bhikhu
APPLICANT: Rohlff, Christian
APPLICANT: Solder, David M.
APPLICANT: Sunderland, P. Trey
APPLICANT: Sunderland, P. Trey
APPLICANT: Sunderland, P. Trey
APPLICANT: Sunderland, Robert Reid
APPLICANT: White, Frost
APPLICANT: Millians, Stephen A.
TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
TITLE OF INVENTION: Alzheimer's Disease
FILE REPERENCE: 2572-1-001 NZ
CURRENT FILING DATE: 2001-04-30
FRICR APPLICATION NUMBER: US 60/194,504
FRICR APPLICATION NUMBER: US 60/253,647
FRICR FILING DATE: 2000-01-03
FRICR FILING DATE: 2000-01-03
FRICR FILING DATE: 2000-04-03
FRICR FILING DATE: 2000-01-03
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                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.7%; Score 24; DB 9; Length 7; Best Local Similarity 57.1%; Pred. No. 1e+06; Matches 4; Conservative 2; Mismatches 1; Indels
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Pred. No. 1e+06;
0; Mismatches
  FILE REFERENCE: MTP-027
CURRENT APPLICATION NUMBER: US/09/998,909
CURRENT FILING DATE: 2001-11-30
                                               PRIOR APPLICATION NUMBER: US 60/250,284 FRIOR FILING DATE: 2000-11-30 NUMBER OF SEQ ID NOS: 14 SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 205, Application US/09826290
Patent No. US20020144668A1
GENERAL INPORMATION:
APPLICANT: Durham, L.Kathryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative (
                                                                                                                                                                                                                                                    TYPE: PRT
GRGANISM: Homo sapiens
US-09-998-909-7
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US-09-826-290-205
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1 YTFELSR 7
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US-09-826-290-370
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LENGTH: 7
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Sequence 370, Application US/09826290 Patent No. US20820164668A1 GRNEAL INFORMATION: APPLICANT: Durham, L.Kathryn

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Sequence 145, Application US/09791393
| Publication No. US200300322004|
| GENERAL INFORMATION: 0. US200300322004|
| GENERAL INFORMATION: DESCRIPTION: DESCRIPTION: DESCRIPTION: DESCRIPTION: Pareth, Rajesh Bhikhu
| APPLICANT: Rohlff, Christian | APPLICANT: Rohlff, Christian | APPLICANT: Rohlff, Christian | TITLE OF INVENTION: Disgnosis and Their Use for | TITLE OF INVENTION: Disgnosis and Treatment of Bipolar Affective Disorder (BAD) | TITLE OF INVENTION: DISGNOSIS and Unipolar Depression | FILE REPRENCE: 2543-1-001 NI | CURRENT APPLICATION NUMBER: US/09/791,393 |
| CURRENT PLIANG DATE: 2000-02-24 | EARLIER APPLICATION NUMBER: GB 0030150.9 |
| EARLIER PLIANG DATE: 2000-12-08 | EARLIER PLIANG DATE: 2000-12-08 |
| BARLIER FILING DATE: 2000-12-08 |
| BARLIER FILING DATE: 2000-12-08 |
| SARLIER FILING DATE: 2000-12-08 |
| SOUTHARE: FREED for Windows Version 4.0 |
| SEQ ID NO 145 | FREED FOR WINDOWS VERSION | TOTAL OF THE CONTROL APPLICANT: White, Frost
APPLICANT: White, Frost
APPLICANT: White, Frost
APPLICANT: Williams, Stephen A.
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: Alzheimer's Disease
FRIOR APPLICATION NUMBER: US 60/194,504
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-011-28
NUMBER OF SEQ ID NOS: 492
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.7%; Score 24; DB 9; Length 7; 57.1%; Pred. No. 1e+06; 1; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.7
Best Local Similarity 57.1
Matches 4; Conservative
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US-10-Z64-309-460

Sequence 460, Application US/10264309

Publication No. US20040022794A1

GENERAL INFORMATION:
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: FRIEDMAN, DAVID M.
APPLICANT: ROHLFF, CHRISTIAN
APPLICANT: STORES, B. M. CHAEL
APPLICANT: STORES, HOLLY D.
APPLICANT: WILLIAMS, STEPHEN A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND TREATMENT OF ALZHEIMER'S DISEASE
FILE REFERENCE: POA-002.01
CURRENT APPLICANTION NUMBER: US/10/264,309
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 491
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: STIGRE, HOMER R.
APPLICANT: STIGRE, HOMER R.
APPLICANT: SUNDERLAND, P. TREY
APPLICANT: TOWNSEND, ROBERT R.
APPLICANT: WHITE, W. PROST
APPLICANT: WILLIAMS, STEPHEN A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND JUSES THEREFOR,
TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
FILE REFERENCE: POA-002.01
CURRENT APPLICATION NUMBER: US/10/264,309
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: 60/326,708
PRIOR PLING DATE: 2001-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.7%; Score 24; DB 16; Length 7; 71.4%; Pred. No. 1e+06; ive 0; Mismatches 2; Indels
                                                                                Application US/10264309
5. US20040022794A1
                                                                             Sequence 131, Application US/1026.
Publication No. US20040022794A1
GENERAL INFORMATION:
APPLICANT: PURHAM, L. KATHRYN
APPLICANT: RIBDMAN, DAVID L.
APPLICANT: KIMMEL, ILDA H.
APPLICANT: PAREKH, RAJESH B.
APPLICANT: PAREKH, RAJESH B.
APPLICANT: ROHLFF, CHRISTIAN
APPLICANT: SOHLFF, CHRISTIAN
APPLICANT: SINTER, BAYID M.
APPLICANT: SONYER, PETER J.
APPLICANT: SOARES, HOLLY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 491
SOFTWARE: Patentin Version 2.1
ESQ ID NO 131
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Best Local Similarity 71.4
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-131
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US-10-264-309-460
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                                                         KESULT 6
US-09-791-389-145

Sequence 145, Application US/09791389

Sequence 145, Application US/09791389

Publication No. US20030032773A1

GENERAL INFORMATION:
APPLICANT: Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Terrett, Jonathan Alexander
APPLICANT: Trerett, Jonathan Alexander
APPLICANT: Trerett, Jonathan Alexander
APPLICANT: Tyson, Kerry Louise
ITILE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
ITILE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder
ITILE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder
ITILE OF INVENTION: Diagnosis and Onjuglar Depression
ITILE OF INVENTION NUMBER: US/09/791,389
CURRENT APPLICATION NUMBER: GB 0004412.3
PRIOR PELING DATE: 2000-02-24
PRIOR PELING DATE: 2000-12-08
PRIOR PELING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/254,830
PRIOR PELING DATE: 2000-12-12
NUMBER OF SEC ID NOS: 308
SOFTWARE: FastSEQ for Windows Version 4.0
IRMATH. 100 145
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APPLICANT INNOGRETICS N.V.
TITLE OF INVENTION: Methodogical Diseases
TITLE OF INVENTION: Methodogical Diseases
FILE REPERBNCE: 11362.0038.NPUS01.
CURRENT APPLICATION NUMBER: US/10/601,100
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 602447121.1
PRIOR PLILING DATE: 2002-06-21
PRIOR FILING DATE: 2002-06-21
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin version 3.2
SEQ ID NO 105
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Publication No. US20040072261A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
COGANISM: homo sapien
US-09-791-389-145
1 YTFELSR 7
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1 YTFELSR 7
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Gaps . 0

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; OTHER INFORMATION: A conserved sequence between Region 2 in IL-22 and IL-10 US-10-238-965-4
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Fatent No. US20020049153A1

GENERAL INFORMATION:

APPLICANT: Bridon, Dominique P.

APPLICANT: Ezzin, Alan M.

APPLICANT: Ezzin, Alan M.

APPLICANT: Leblanc, Anouk

APPLICANT: Leblanc, Anouk

APPLICANT: Leblanc, Anouk

APPLICANT: Leblanc, Anouk

APPLICANT: St. Pierre, Serge

TITLE OF INVENTON: LONG LASTING INSULINOTROPIC PEPTIDES

FILE REFERENCE: 500662001610

CURRENT APPLICATION NUMBER: US/09/876,388

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 209623,618

PRIOR FILING DATE: 2000-09-05

PRIOR FILING DATE: 2000-05-17
                                                                                                                                                                                                                                                                                                                                                           Score 20; DB 14; Length 7; Pred. No. 1e+06; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Nagen, Ronaldo A.P.
APPLICANT: Nagen, Ronaldo A.P.
APPLICANT: Renauld, Jean-Christophe
APPLICANT: Renauld, Jean-Christophe
APPLICANT: Dolikarpov, Igor
TITLE OF INVENTION: Cryetal Structure of Interleukin-22
TILE PERERENCE: LUD-572 US
CURRENT APPLICATION NUMBER: US/10/238,965
CURRENT APPLICATION NUMBER: 60/317,937
PRIOR APPLICATION NUMBER: 60/317,937
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-11-27
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 7
LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.6%; Score 20; DB 15; Length 7; 100.0%; Pred. No. 1e+06; tive 0; Mismatches 0; Indels
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4, Application US/10238965; Publication No. US20040002586A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     50.08;
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                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Brassica oleracea
US-10-234-026-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.6
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0
Matches 3; Conservative
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2 TIELSK 7
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US-09-876-388-6
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; OTHER INFORMATION: A conserved sequence between Region 2 in IL-22 and IL-10 US-10-050-552A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Publication No US20030097679A1

### GENERAL INFORMATION:

### APPLICANT: Widams Interuniversitair Instituut voor Biotechnol APPLICANT: Guy Jerome Corneel Bauw

### APPLICANT: Guy Jerome Corneel Bauw

### APPLICANT: Marc Charles Ernest Van Montagu

### APPLICANT: Marc Charles From Montagu

### APPLICANT: Marc Charles Ernest Van Montagu

#### APPLICANT: Marc Charles Van Mo
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| US-110-US-12-2A-4-4|
| Publication No. US20020187512A1
| GENERAL INFORMATION:
| APPLICANT: Nacement Ronaldo A.P. |
| APPLICANT: Colau, Didier |
| APPLICANT: Renauld, Jean-Christophe |
| APPLICANT: Renauld, Jean-Christophe |
| APPLICANT: Polikarpov, Igor |
| APPLICANT: Polikarpov, Igor |
| TITE OF INVENTION: Crystal Structure of Interleukin-22 |
| TITE OF INVENTION: Crystal Structure of Interleukin-22 |
| TITE OF INVENTION: Crystal Structure of Interleukin-22 |
| TITE OF INVENTION: Crystal Structure of Interleukin-22 |
| TILE REPRENCE: LUD-572 US |
| CURRENT APPLICATION NUMBER: 06/317,937 |
| PRIOR FILING DATE: 2001-09-10 |
| PRIOR FILING DATE: 2001-09-10 |
| PRIOR FILING DATE: 2001-11-27 |
| NUMBER OF SEQ ID NOS: 5 |
| SEGTWARE: Patentin version 3.1 |
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                                                                                                                                                                                                                                                                                                           72.7%; Score 24; DB 16; Length 7; 57.1%; Pred. No. 1e+06; 1; Mismatches 1; Indels
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 460
LENGTH: 7
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ORGANISM: artificial sequence
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-10-264-309-460
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Gaps

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OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-10-287-892-6
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PRIOR APPLICATION NUMBER: 09/657,332
PRIOR FILING DATE: 2000-09-07
PRIOR PELING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PACENTIN Ver. 2.1
SEQ ID NO 6
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: June 2, 2004, 19:08:54 Job time: 37.5 secs
                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 50.0
Matches 3, Conservative
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1 FTSDVS 6
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Sequence 6, Application US/10287892
Publication No. US20030108567A1
GENERAL INFORMATION:
APPLICANT: Didon, Dominique P.
APPLICANT: L'Archeveque, Benoit
APPLICANT: Holmes, Darren L.
APPLICANT: Holmes, Darren L.
APPLICANT: Holmes, Darren L.
APPLICANT: St. Pierre, Serge
TITLE OF INVENTION: LONG LASTING SYNTHETIC GLUCAGON LIKE PEPTIDE (GLP-1)
FILE REFERENCE: SO0862001612
CURRENT APPLICATION NUMBER: US/10/287,892
CURRENT FILING DATE: 2002-11-04
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                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic // OTHER INFORMATION: Peptide US-09-876-388-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39, Application US/10105930

Sequence 39, Application US/10105930

Publication No. US20030009018A1

GENERAL INFORMATION:

APPLICANT: Macada, Masatsugu

APPLICANT: Macada, Masatsugu

APPLICANT: Waguchi, No. US20030009018A1iko

TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12

FILE REFERENCE: 06501-1051031

CURRENT APPLICATION NUMBER: US/10/105,930

CURRENT FILING DATE: 2002-03-25

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-03

PRIOR PLING DATE: 1999-09-17

PRIOR PLING DATE: 1999-09-17

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 39

LENGTH: 6

LENGTH: 6
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                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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Pred. No. 1e+06;
2; Mismatches 1; Indels
  PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-05-17
NUMBER: 06/134,406
SOUTWARE: PATENTIN VOY: 2.1
SEQ ID NO 6
ILENGTH: 6
TYPE: PT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0%;
Matches 3; Conservative
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US-10-105-930-39
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Best Local Similarity
Matches 3; Conserv
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1 YTLQI 5
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Sequence

Sequence Sequence Sequence

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Sequence 8, Application US/08222619;
Patent No. 5652352;
GENERAL INFORMATION:
JICHORSTEIN, Henri
APPLICANT: Lichenstein, Henri
APPLICANT: Wurfel, Mark
APPLICANT: Wurfel, Mark
ITILE OF INVENTION: Asmuel
ITILE OF INVENTION: Protein
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.7%; Score 24; DB 1; Length 7; 71.4%; Pred. No. 3e+05; 2; Indels ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,619
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent Operations/RRC
Drive
US-09-522-433B-12
US-09-639-541B-636
US-09-839-542B-650
US-08-136-743B-29
US-08-136-743B-29
US-08-136-743B-54
US-08-136-743B-54
US-08-136-743B-54
US-08-136-743B-55
US-08-136-743B-59
US-08-136-743B-69
US-08-136-743B-69
US-08-136-743B-60
US-08-136-743B-60
US-08-136-743B-60
US-08-136-743B-60
US-08-136-773B-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 91320-1789
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
PCT-US95-04075-8
; Sequence 8, Application PC/TUS9504075
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...LKESSEE: Amgen Center, Pa
STREET: 1840 DeHavilland Dr.
CITY: Thousand Oaks
STATE: California
COUNTRY: U.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
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Best Local Similarity 71.4
Matches 5; Conservative
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MOLECULE TYPE: peptide
US-08-222-619-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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         STRANDEDNESS:
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US-08-222-619-8
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                                                                                                                                                                                                        June 2, 2004, 18:56:07; Search time 15.5 Seconds (without alignments) 23.315 Million cell updates/sec
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Sequence 6,
Sequence 21
Sequence 22
Sequence 55
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Sequence 6
Sequence 6
Sequence 6
Sequence 7
Sequence 7
Sequence 7
Sequence 2
Sequence 2
Sequence 2
Sequence 5
Sequence 5
Sequence 6
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11. \c9T2_6/\text{ptodata}2/\text{iaa}/5A_\text{COMB.pep:*}
12. \c9T2_6/\text{ptodata}2/\text{iaa}/5B_\text{COMB.pep:*}
13. \c9T2_6/\text{ptodata}2/\text{iaa}/6A_\text{COMB.pep:*}
14. \c9T2_6/\text{ptodata}2/\text{iaa}/6B_\text{COMB.pep:*}
15. \c9T2_6/\text{ptodata}2/\text{iaa}/\text{PCTUS} \cOMB.pep:*}
16. \c9T2_6/\text{ptodata}2/\text{iaa}/\text{PCTUS} \cOMB.pep:*}
17. \c9T2_6/\text{ptodata}2/\text{iaa}/\text{packflles1.pep:*}
18. \c9T2_6/\text{ptodata}2/\text{iaa}/\text{packflles1.pep:*}
19. \c9T2_6/\text{ptodata}2/\text{iaa}/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{ptodata}2/\text{p
                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US - 09 - 423 - 468A-6

US - 08 - 122 - 6194.2

US - 08 - 136 - 743B - 55

US - 08 - 136 - 743B - 55

US - 09 - 623 - 618B-6

US - 09 - 623 - 618B-6

US - 09 - 627 - 312A-6

US - 09 - 627 - 618B-6

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US - 09 - 627 - 618B-7

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US - 09 - 223 - 623 - 623

US - 09 - 627 - 332A-7

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US - 09 - 118 - 743B - 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                          protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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33
1 PTLEISR 7
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0 seq length: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
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                                                                                                                                                                                                                     Run on:
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No.
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Gaps

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Sequence 21, Application US/08222619
Patent No. 5652352
GENERAL INFORMATION:
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Sequence 6, Application US/09423468A

Sequence 6, Application US/09423468A

Patent No. 6469149

GENERAL INFORMATION:

APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol

APPLICANT: Guy Jerome Corneel Bauw

APPLICANT: Guy Jerome Corneel Bauw

APPLICANT: Mark William Davey

APPLICANT: Marc Charles Ernest Van Montagu

ITLE OF INVENTION: PRODUCTION OF ASCORBIC ACID IN PLANTS

FILE REFERENCE: DECLES. 001APC

CURRENT APPLICATION NUMBER: US/09/423,468A

CURRENT FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: NL 1006000

PRIOR APPLICATION NUMBER: NL 1006000

PRIOR FILING DATE: 1997-06-07

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 6

LENGTHA: 7

LENGTHA: 7

LENGTHA: 7

LENGTHA: 7
APPLICANT: AMGEN INC;
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ANGEN Center, Patent Operations/RRC
STREST: 1640 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUMTRY: U.5.
ZIP: 91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.6%; Score 20; DB 4; Length 7; 50.0%; Pred. No. 3e+05; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 24; DB 5; Length 7; Pred. No. 3e+05;
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.7%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERASTICS:
LENGTH: 7 amino acids
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Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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Best Local Similarity
Matches 5, Conserva
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2 TIELSK 7
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US-08-222-619-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
APPLICANT: Lichenstein, Henri
APPLICANT: Lyons, David
APPLICANT: Lyons, David
APPLICANT: Wurfel, Mark
APPLICANT: Wright, Samuel
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: AMGEN Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ANGEN INC.
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: Angen Center, Patent Operations/RRC
STREET: Thousand Oaks
STATE: COUNTRY: U.S.
                                                                                                                                                                                      PUDRESERSE: Amgen Center, Patent Operations/RRC STREET: 1840 DeHavilland Drive CITY: Thousand Oaks STATE: 2011/Cornia CALIGORIA CALIGORIA CALIGORIA CALIGORIA COUNTRY: U.S. 2178: 91320-1789 COMPUTER: FLOPPY disk COMPUTER: PAPLICATION DATA: APPLICATION NUMBER: US/08/22,619 FILING BATE: APPLICATION NUMBER: US/08/22,619 FILING BATE: CLASSIFICATION: 435 INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 91320-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US95-04075-21; Sequence 21, Application PC/TUS9504075; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local_Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: un
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APPLICANT: Yakubu-Madus, Fatima E.
APPLICANT: Yakubu-Madus, Fatima E.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENTS OF
TITLE OF INVENTION: GLUCAGON-LIKE INSULINOTROPIC PEPTIDE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company/RSM
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: IN
                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Ribonucleotide reductase inhibitor peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.6%; Score 19; DB 3; Length 7; 60.0%; Pred. No. 3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: residue 1: MOD_RES: ACETYLATION
US-09-040-216-28
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,731
FILING DATE:
TITLE OF INVENTION: RIBONUCLECTIDE REDUCTASE
FILE REPERENCE: 9596-6301
CURRENT APPLICATION NUMBER: US/09/040,216
CURRENT FILING DATE: 1998-03-17
FARLIER APPLICATION NUMBER: 08/919,748
EARLIER PILING DATE: 1997-08-28
EARLIER FILING DATE: 1996-08-28
EARLIER FILING DATE: 1996-08-30
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PATENTIN VEY: 2.0
SOFTWARE: PATENTIN VEY: 2.0
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Patent No. 5574008
GENERAL INFORMATION:
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TELEPRAX: 317-27-1917
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Maciak, Ronald S.
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.6
Best Local Similarity 60.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                            Sequence 55, Application US/08136743B
Patent No. 5459063
GENERAL INFORMATION:
APPLICANT: Barry S. Cooperman, Harvey Rubin,
APPLICANT: Jerome Salem, and Alieon L. Fisher
TITLE OF INVENTION: "Plasmodium falciparum Ribonu-
TITLE OF INVENTION: Thereof"
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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GENERAL INFORMATION:
APPLICANT: COOPERMAN, ET AL., BARRY
TITLE OF INVENTION: PEPTIDES, PEPTIDE ANALOGS, PEPTIDOMIMETICS, AND OTHER
TITLE OF INVENTION: SMALL MOLECULES USEFUL FOR INHIBITING THE ACTIVITY OF
                                                                                                                                              Gaps
                                                                                                                                              ö
                                                                                            Score 19; DB 5; Length 6;
Pred. No. 3e+05;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.6%; Score 19; DB 1; Length 7; 60.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE The University of Pennsylvania STREET: Suite 330
STREET: State 330
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19104-3246
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KD
COMPUTER: IBM PS/2
COPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,743B
FILING DATE: 10/14/93
CLASSIFICATION: 10/14/93
CLASSIFICATION NUMBER: 30,480
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 3957-10
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
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US-09-040-216-28
; Sequence 28, Application US/09040216
; Sequence 28, Application US/09040216
; Sequence 18, Application US/09040216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (215) 568-8383
TELERAX: (215) 568-5549
TELEX: NO. 5459063e
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                         Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-04075-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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Best Local Similarity
Matches 3; Conserv
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1 FTLDL 5
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Gaps
                                      FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic;
; OTHER INFORMATION: Peptide
US-09-657-332A-6
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                                                                                                                                                                                                                                                                          .
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Sequence 4, Application PC/TUS9510793

GENERAL INFORMATION:

APPLICANT: Vakubu-Madus, Patima E.

TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENTS OF

TITLE OF INVENTION: GIUCAGON-LIKE INSULINOTROPIC PEPTIDE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSED: Eli Lilly and Company/RSM

STREET: Lilly Corporate Center

CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAREAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: L'Archeveque, Benoit
APPLICANT: Ezin, Alan M.
APPLICANT: Ezin, Alan M.
APPLICANT: Ezin, Alan M.
APPLICANT: Borin: Barren L.
APPLICANT: Holbanc, Anouk
APPLICANT: Leblanc, Anouk
APPLICANT: St. Parren Lows Lasre
TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
TITLE REPERENCE: 500862001610
CURRENT APPLICATION NUMBER: 09/623,618
PRIOR APPLICATION NUMBER: 09/623,618
PRIOR APPLICATION NUMBER: PCT/US00/13563
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR PLING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR PLING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR PLING DATE: 1999-05-17
PRIOR PLING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR PLING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR PLING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR PLING DATE: 1999-05-17
PRIOR PLING DATE: 1999-05-17
                                                                                                                                                                                                    Score 18; DB 4; Length 6;
Pred. No. 3e+05;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                   1; Indels
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Pred. No. 3e+05;
2; Mismatches 1; Indels
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       ORGANISM: Artificial Sequence
                                                                                                                                                                                                        54.5%;
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Best Local Similarity 50.0
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserva
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FTSDVS 6
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1 FTSDVS 6
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US-09-876-388-6
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PCT-US95-1
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Betent No. 6514500

GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Bridon, Dominique P.
APPLICANT: L'Archeveque, Benoit
APPLICANT: L'Archeveque, Benoit
APPLICANT: Lebanar. Anouk
APPLICANT: Lebanar. Anouk
APPLICANT: St. Pierre, Gerge
TITLE OF INVENTION: LONG LASTING SYNTHETIC GLUCAGON LIKE PEPTIDE (GLP-1)
FILE REPRENENCE: 50086201600
CURRENT FILING DATE: 2010-09-10
CURRENT FILING DATE: 2010-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR PILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: Bridon, Dominique P.
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Ezrin, Alan M.
APPLICANT: Ezrin, Alan M.
APPLICANT: Holmes, Darren L.
APPLICANT: Holmes, Darren L.
APPLICANT: St. Pierre, Serge
TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
FILE REREERENT S.
FORENT APPLICATION NUMBER: US/09/623,618B
CURRENT APPLICATION NUMBER: POT/US00/13563
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR PILING DATE: 1099-10-15
PRIOR PILING DATE: 1999-10-15
PRIOR PILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 6
LENG
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09623618B
Patent No. 6329336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0
Matches 3; Conservative
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1 FTSDVS 6
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1 FTSDVS 6
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US-09-623-618B-6
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Gaps
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Patent No. 6387616
FAREAL INFORMATION:
APPLICANT: Ozellus, Laurie J.
APPLICANT: Breakfield, Xandra O.
TITLE OF INVENTION: TORSIN, TORSIN GENES, AND METHODS OF USE
FILE REFERENCE: MGH-11849A2
CURRENT APPLICATION NUMBER: US/09/218,363
CURRENT APPLICATION NUMBER: 09/099,454
EARLIER FILING DATE: 1998-06-18
EARLIER PILING DATE: 1998-06-18
EARLIER FILING DATE: 1998-06-18
EARLIER FILING DATE: 1997-06-19
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09623618B
Patent No. 6329336
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezin, Alan M.
APPLICANT: Ezin, Alan M.
APPLICANT: L'Archeveque, Benoit
APPLICANT: Ezin, Alan M.
APPLICANT: Leblanc, Anouk
APPLICANT: Looper, Serger
TITLE OF INVENTION: LONG LASTING
FILE REFERENCE: 500862001620
CURRENT FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 35
SOFTHARE: PASESEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 7
                                                                                               Score 18; DB 1; Length 7;
Pred. No. 3e+05;
2; Mismatches 1; Indels
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S4.5%; Score 18; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 38+05;
Matches 3; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                  Query Match
Best Local Similarity 50.0%;
Matches 3; Conservative
  / TOPOLOGY: linear
// MOLECULE TYPE: peptide
US-08-297-731-5
                                                                                                                                                                                                    1 FTLEIS 6
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2 FTSDVS 7
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2 FTSDVS 7
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US-09-218-363-23
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APPLICANT: Yakubu-Madus, Fatima E.
APPLICANT: Yakubu-Madus, Fatima E.
APPLICANT: Yakubu-Madus, Fatima E.
APPLICANT: Yakubu-Madus, Fatima E.
TITLE OF INVENTION: GLUCAGON-LIKE INSULINOTROPIC PEPTIDE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company/RSM
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 5; Length 6;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
ZIP: 46285

COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTE: IBM PC compatible
COMPUTE: OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10793
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPHONE: 317-276-1664
TELEPHONE: 317-276-1664
TELEPHONE: 317-276-1664
TELEPHONE: 317-276-1664
TELEPHONE: 317-276-1664
TELEPHONE: 317-276-1664
TELEFAX: SEQUENCE CHARACTERISTICS:
TENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Maciak, Ronald S.
REGISTRATION WIMBER: 35,262
REFERENCE/DOCKET UNBER: X963
TELEPHONE: 317-276-1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0
Matches 3; Conservative
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide PCT-US95-10793-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FTSDVS 6
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; TYPE: PRT ; ORGANISM: Homo sapien US-09-218-363-23

Query Match 54.5%; Score 18; DB 4; Length 7; Best Local Similarity 75.0%; Pred. No. 3e+05; Matches 3; Conservative 1; Mismatches 0; Indels

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0; Gaps

Search completed: June 2, 2004, 19:01:06 Job time: 15.5 sec8

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June 2, 2004, 18:54:42; Search time 13 Seconds (without alignments) 51.795 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                        457
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                   283366 segs, 96191526 residues
                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                   US-09-712-819D-13
31
1 LTLKLSR 7
                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0 Maximum DB seq length: 7
                                                                                                                                                                                   Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                              Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Description	ribosomal protein			flagellar protein	cytotoxic T-lympho	peptidyl-dipeptida	phosphonoacetaldeh	glycoprotein compo	DNA topoisomerase	major fat-globule	hypothetical prote	hypothetical prote	н	Ig mu chain D regi	relaxing	sex pheromone CCF1	ĭ	pullulanase (EC 3.	copper resistance	T-cell receptor be			T-cell receptor be	surface protein te	dnaA protein - Pse	28K ubiquitin-immu	MHC H2-L antigen -	T-cell receptor be	_
SU CI	S19630	T1389		E4	149424	JN0859	A28709	田		щ					ECMUCR				C41225					86923	B3483	A43766	I6554	PT051	PT066
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C;Species: mitochondrion Lampetra fluviatilis (river lamprey mitochondrion (f C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
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C;Species: mitorion fluoresevies (river lamprey)
R;Delarbre, C; Barriel, V; Tillier, S; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the A;Reference number: Z17775; MUJD:97398704; PMID:9254918
A;Reference number: Z17775; MUJD:97398704; PMID:9254918
A;Residues: T3 < CBLS
A;Residues: T3 < CBLS
A;Residues: T3 < CBLS
A;Coss-references: EMBL:Y09528; NID:92340016; PIDN:CAA70721.1; PID:94379123
A;Gennetics:
A;Gennetics:
A;Gennetics: mitochondrion; oxidoreductase

T13892

Gaps . 0 Query Match 35.5%; Score 11; DB 3; Length 3; Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0; Indels

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C;Accession: E48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1933
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-p II-like sequences.
A;Reference number: A48394; MUID:93250576; PMID:8485470
A;Accession: B48394
A;Status: preliminary
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: intestine C; Comment: The carboxyl-terminus is essential for the protein's expression of angioter. C; Superfamily: bradykinin-torentiating peptide C; Superfamily: bradykinin-converting enzyme inhibitor C; Keywords: angiotensin-converting enzyme inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A28709 ... Moos, M.; Mariano, P.S.; Dunaway-Mariano, D. Biochemistry 27, 2229-2234, 1988 A;Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidenc
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C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
                                                                                                                                                                                                            peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito
C;Species: Sarda orientalis (striped bonito)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: UNO889
R;Matsumura, N; Filji, M:, Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A;Reference number: JNO859; MUD:94080036; PMID:7764272
A;Accession: NNO859
A;Molecule type: protein
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C;Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
      Gaps
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A;Accession: A28709
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <0LS>
         Mismatches
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      2; Conservative
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                                                                                                                             hypothetical protein c4 - loblolly pine
(Species: Pinus taeda (loblolly pine)
(Species: Pinus taeda (loblolly pine)
(Species: 18-Peb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
(SAccession: T46627
(Stane). S.; Purkyea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
(Stane). S.; Purkyea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
(Submitted to the EMBL Data Library, July 1995
(A)Pescription: Cloning of a chitinase homolog which lacks chitin binding sites and is do A)Reference number: 223105
(A)Reference number: 223105
(A)Residues: preliminary; translated from (GB/EMBL/DDBJ
(A)Residues: 1-4 cHAA)
(A)Residues: 1-4 cHAA)
(A)Residues: L-4 cHAA)
(A)Residues: L-4 cHAA)
(B)RESPERTIMENTAL SOURCE: Strain s6FTZX86FT3; 8 month seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              flagellar protein filk - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 24-Uul-1992 #sequence_revision 24-Uul-1992 #text_change 30-Sep-1993
C;Accession: E42364
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
A; Bacteriol. 173, 3564-3572, 1991
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seq
A;Reference number: A42364; MUID:91258342; PMID:1646201
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C; Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 05-Nov-1999
C; Accession: 149424
Mamm. Genome 5, 349-355, 1994
A; Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A; Reference number: 148934; MUID:94319082; PMID:8043949
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C.Species: Mus spretus (western wild mouse)
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A;Molecule type: DNA
A;Residues: 1-6 - KRES-
A;Cross-references: EMBL:U05745; NID:G497084; PIDN:AAB60481.1; PID:G642831
C;Keywords: hydrolase; serine proteinase
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Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0;
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66.7%; Pred. No. 2.8e+05;
iive 1; Mismatches 0;
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Best Local Similarity 66.7
Matches 2; Conservative
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A, Molecule type: DNA
A, Residues: 1-5 < VOG>
A, Cross-references: GB: M62408
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hypotherical protein - parsley
hypotherical protein - parsley
Cispecies: Petroselinum crispum (parsley)
Cispecies: 20-8ep-1999 #sequence_revision 20-8ep-1999 #text_change 21-Jul-2000
Cispecies: 20-8ep-1999
Richer, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Reference number: Z18261; MUID:98265918; PMID:9604882
A;Recession: T1840;
A;Accession: T1840;
A;Accession: T1840;
A;Accession: T1840;
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-5 < KIR>
A;Residues: 1-5 < KIR>
A;Residues: 1-5 < KIR>
A;Cross-references: RMBL:Y10810; NID:g3336904; PIDN:CAA71769.1; PID:g3336905
A;Experimental source: ssp. Hamburger Schnitt
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Eur. J. Biochem. 158, 505-510, 1986

A,Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA A,Tetle: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA A,Accession: 140505

A,Accession: 140505

A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Mochecule type: DNA
A,Residues: 1-4 <RES>
A,Residues: 1-4 <RES>
A,Cross-references: EMBL:X04193; NID:g40233; PIDN:CAA27783.1; PID:g580944
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C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
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Cipate: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-196/cipate: 05-Sep-1997 #text_change 05-Nov-1997 #text_change 05-Nov-1997 #text_change 05-Sep-1998 #tex
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Pred. No. 2.8e+05;
1; Mismatches 0; Indels
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32.3%;
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Bochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.
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C;Species: Bacillus stearothermophilus
C;Bate: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C;Accession: I40505
R;Waye, M.M.; Winter, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA topoisomerase II alpha - Chinese hamster (fragment)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
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C.Species: Cavia porcellus (guinea pig)
C.Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C.Accession: B48394
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A;Residues: 1-7 <MAT>
A;Experimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131450)
C;Keywords: glycoprotein
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RN94, S. W.; Eder, U.P.; Schnipper, L.B.; Chan, V.T.W.
J. Biol. Chem. 270, 25550-25859, 1995
A;Title: Molecular cloning and characterization of the p. A;Ecreane number: I48086, MUID:96029684; PMID:7592770
A;Accession: I48086
A;Cattus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-7 <RES>
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Ig mu chain D region (D23) - mouse
C.Species: Mus musculus (house mouse)
C.Species: We musculus (house mouse)
C.Accession: B33932
R.Baccala, R.: Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
R.Baccala, R.: Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
R.Baccala, R.: Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
R.Baccala, R.: Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
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R.Baccala, R.: Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
R.Baccala, R.: Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
R.Baccala, R.: Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
R.Baccala, R.: Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
R.; Reference number: A33932; MUD:8928283; PMID:2499887
A.; Reference number: A33932; MUD:8928283; PMID:2499887
A.; Molecule type: mRNA
A.; Molecule type: mRNA
A.; Coss. references: GB:M27107
C; Keywords: immunoglobulin
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Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
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SEQUENCE.
MEDLINE=89008313; PubMed=3139658;
MOTI M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
Adsit J.C., Dunny G.M., Suzuki A.;
Structure of CCF10, a poptide sex pheromone which induces
conjugative transfer of the Streptococcus faecalis tetracycline
resistance plasmid, pCF10.";
J. Biol. Chem. 263:14574-14578 (1988).
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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BIOA_CITFR
UF01_MOUSE
ACPH_RABIT
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P58706 anthopleura P01858 home sapien P31425 bothrops in P41853 artioposthi P01373 periplaneta P58267 litoria rub P82072 litoria rub P13973 escherichia P82655 lactobacill P41966 moniezia ex P41495 sarcophaga	s AA.	01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sequence update) 01-MAR-1989 (Rel. 10, Last annotation update) 02-MAR-1989 (Rel. 10, Last annotation update) 03-ch-relaxing peptide (CARP) 03-ch-relaxing peptide (CARP) 03-ch-relaxing peptide (CARP) 03-ch-relaxing peptide (MARP) 03-ch-relaxing peptide (MARP) 03-ch-relaxing peptide (MARP) 04-ch-relaxing peptide (MARP) 05-ch-relaxing peptide (MARP) 06-ch-relaxing pept	Kawahara A., Shimamoto N., Wytilus pedal ganglia."; oth potentiating (contraction) ts on the anterior byssus N. 669DB0 CRC64;	DB 1; Length 7; 1.4e+05; hes 0; Indels 0; Gaps 0;
PYRI ANTEL     TUFF HUMAN     PARP BOTIN     PARP ARTTR     PSK DAUCA     PSK DAUCA     RE31 LITRU     RB32 LITRU     TRM3 ECOLI     TRM3 ECOLI     TRM3 ECOLI     ASP2 LACSN     PARP MONEX     TWOF SARBU	ALIGNMENTS PRT; 7	Created) Last sequence update) Last annotation update) (CARP) USSE1). Husse1). Husca; Bivalvia; Pteri Mytilus.	I., from ts b iffec iffec	Score 10; Pred. No. 1; Mismatc
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	STANDAR	01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last seq 01-MAR-1989 (Rel. 10, Last ann Catch-relaxing peptide (CARP). Wytilus edulis (Blue mussel). BNRATYOTE, Metazoa; Mollusca; Mytiloidea; Mytilidae; Mytilus NCBL TAXID=6550;	SEQUENCE.  MEDLINE=88052022; PubMed=3676797; MITTER T., Kubota I., Takabatake Muncoka Y.; Cacch-relaxing peptide isolated Brain Res. 422:374-376(1987)!- FUNCTION: This peptide exhibi and inhibitory (relaxation) e Ferractor muscle. Ferractor muscle. Ferractor mascle. Formone; Amidation. MOD Res. Amidation.  7 AMID SEQÜENCE 7 AA; 831 MW; 673407	32.3%; Similarity 66.7%; 2; Conservative LKL 5 IRL 7 LRL 7
	CARP_MYTED LD CARP_MYTED AC P10420;	01-MAR-1989 (Rel 01-MAR-1989 (Rel 01-MAR-1989 (Rel Catch-relaxing p Mytilus edulis ( Enkaryota, Metaz Mytiloidea, Myti NCBL_TAXID=6550,	SEQUENCE. MEDLINE=88052022; PHIREL T., Kubota I. Muneoka Y.; Kubota I. Muneoka Y.; Kubota I. Muneoka Y.; Kubota I. Catch-relaxing pepiatan Res. 422:374-'	Query Match Best Local Simi Matches 2; 3 LKL
	RESULT CARP_M ID _C	PD D D D D D D D D D D D D D D D D D D	SO CCC RAPARED SO STANDARD SO STANDARD SO CCC STANDARD SO CCC STANDARD SO STAN	oy Age Co

Gaps

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Wabhitz P.A., Bowle J.H., Tyler M.J., Wallace J.C., "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-92195954; PubMed-1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
Identification of RPamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
-!- SIMILARITY: Belongs to the FARP (FWRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Litoria rubella (Desert tree frog).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;

Amphibla, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae;

Pelodryadinae, Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FARS HIRME STANDARD; PRT; 7 AA.

PASS 44
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRPamide-like neuropeptied GGKWMRP-amide.
Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Ariynchobdellida; Hirudiniformes; Hirudinidae; Hirudinea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h Similarity 33.3%; Score 8; DB 1; Length 5; Similarity 33.3%; Pred. No. 1.4e+05; 1; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                        Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Skin.
Amphibian defense petide; Amidation.
MOD RSS
SEQUENCE 5 AA, 616 MW; 61F2D1A059A00000 CRC64;
                                                                                                                                                                7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;
                                                                                                                                                                                                                                        29.0%; Score 9; DB 1; Lilarity 66.7%; Pred. No. 1.4e+05; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
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                    Maize-2DPAGE; P80630; COLEOPTILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family.
Neuropeptide; Amidation.
MOD_RES 7 7
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Best Local Similarity
Matches 1; Conserv
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                                                        MaizeDB; 123956; -
NON_TER 1
NON_TER 7
SEQUENCE 7 AA;
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28-FEB-2003 (
10-OCT-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
E104_LITRU
ID E104_LITRU
AC P82100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rubella.";
                                                                                                                                                                                                                                            Query Match
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FARS_HIRME
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Matches
                    RAFFS
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Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,

Pernollet J.-C., Zivy M., de Vienne D.;

"The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oxidase from Alcaligenes sp.";
J. Blochem. 88:197-203(1980).
-!- CATALVITC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2)
Oxidoreductase.
-!- FUNCTION: CCP10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMOLYSIN PLASMID PCF10.
PIR, A30812; A30812.
Pheromone 7 AA, 790 MW, 72C9D2C731B2C740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-!- MISCELLANEOUS: On the 2D-gel the determined pl of this unknown
protein is: 6.0, its MM is: 30.0 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.

BEDLINE=81006769; PubMed=6997283;
Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;

Identification and properties of the prosthetic group of choline
                                                                                                                                                                                                                                                                                                                    ö
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01-OCT-1996 (Rel. 34, Last sequence update)
15-YAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choline oxidase (EC 1.1.3.17) (Fragment).
Alcaligenes sp.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                    32.3%; Score 10; DB 1; Length 7; illarity 66.7%; Pred. No. 1.4e+05; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA; 839 MW; 7415B1E457644AC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.0%; Score 9; DB 1; Le
100.0%; Pred. No. 1.4e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHOX ALCSP STANDARD; PRT; 7 AA. P16101; 01-APR-1990 (Rel. 14, Last sequence update) 01-APR-1990 (Rel. 14, Last annotation update) 01-APR-1990 (Rel. 14, Last annotation update)
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NCBI_TaxID=512;
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Best Local Similarity 100.
Matches 2; Conservative
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Matches 2; Conserv
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Zea mays (Maize)
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2 VTL 4
                                                                                                                                                                                                                                                                                                                                                                                        1 LTL 3
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UC24_MAIZE
ID UC24_MAIZE
P80630;
COT-199'
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Gaps

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EMBL; M62812; -; NOT_ANNOTATED_CDS.
Luminescence; Ligase.
NON TER
SEQUENCE 3 AA; 374 MW; 6AA33030
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                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=546;
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1 IK 2
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Matches
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01-MAR-1992 (Rel. 21, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site for the lux operon..;
J. Bacteriol. 172:6797-6802 (1990).
-!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
IT IS A COMPONENT OF THE FAITY ACID REDUCTASE COMPLEX RESPONSIBLE FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
                                          Gaps
                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP cyclohydrolase I. This inhibition is reversed by L-phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=91072226; PubMed=2254256;
Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
"A new Vibrio fischeri lux gene precedes a bidirectional termination
                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TäxID=668;
                                                                                                                                                                                                                                                                              Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                   Query Match 25.8%; Score 8; DB 1; Length 7; Best Local Similarity 50.0%; Pred. No. 1.4e+05; Matches 2; Indele Matches 2; Indele
                                                                                                                                                                                                                                                                                                                                                                                                               Score 8; DB 1; Length 7; Pred. No. 1.4e+05; 1; Mismatches 1; Indels
 858 MW; 69D4068B53387810 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            7 AA; 806 MW; 71B5B057273B4700 CRC64;
                                                                                                                                 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AA.
                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                            Submitted (AUG-1998) to Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Similarity 50.0%;
2; Conservative
                                                                                                                                  STANDARD;
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                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
7 AA;
                                                                                                                                                                                                                                      NCBI_TaxID=10090
                                                             4 KLSR 7
                                                                               3 KYMR 6
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                                                                                                                                                                                                                                                         SEQUENCE.
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                   Cowthorne M
                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIBFI
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
LUXE VIBFI
                                                                                                                        MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
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                                                                                                              RESULT 7
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SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
--- CATALYTIC ACTIVITY: APP + an acid + protein = AMP + diphosphate + an acyl-protein thiolester.
--- PATHWAY: Bioluminescent fatty acid reduction system; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE 89006280; PubMed=2971595;
Shiuan D., Campbell A.;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli, citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211 (1988).
-I. CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Adenosylmethionin-9-amino-7-oxononanoate aminotransferase
(RC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA aminotransferase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Citrobacter freundii.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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larity 50.0%; Pred. No. 1.4e+05;
Conservative 1; Mismatches 0; Indels
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PIR; 140697; 140697.
PIR; 140697; 140697; A.
PROSITE; PS00600; AA TRANSFER_CLASS_3; PARTIAL.
PROSITE; PS00600; AA TRANSFER_CLASS_3; PARTIAL.
Prictin biosynthesis; Transferase; Aminotransferase; NOV_TER.
SOUN_TER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AA; 374 MW; 6AA330300000000 CRC64;
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Gaps

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Flengerud R., Skjeldal L.; Two-dimension and N-terminal Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5."; Electrophoresis of proteins from Clostridium pasteurianum W5."; -1- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-010-1998 (Rel. 36, Created)
15-010-1998 (Rel. 36, Last sequence update)
15-010-1998 (Rel. 36, Last annotation update)
Uhknown protein F6 from 2D-page (Fragment).
Clostridium pasteurianum.
Bacteria; Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Capaid assembly and DNA maturation protein (Virion protein UL38)
(Capaid protein VP19C) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r Match 22.6%; Score 7; DB 1; Length 6; Local Similarity 25.0%; Pred. No. 1.4e+05; les 1; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                           'Match 22.6%; Score 7; DB 1; Length 6; Local Similarity 33.3%; Pred. No. 1.4e+05; les 1; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=91101287; PubMed=1846198;
Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herpes simplex virus (type 1 / strain KOS).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Appaherpesvirinae; Simplexvirus.
NCBI TaxID=10306;
                                                                                                 InterPro; IPR002471; Pept S9 AS.
PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
Hydrolase; Acetylation.
Hydrolase; Acetylation.
ACETYLATION.
NON TER
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6
SEQÜENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;
-1- SUBUNIT: Homotetramer.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: Belongs to peptidase family S9C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AA.
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STRAIN=W5;
MEDLINE=98291870; PubMed=9629918;
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                                                          PIR; A49792; A49792.
MEROPS; S09.004; -.
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1 MER 3
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VP19_HSV1K
ID VP19_HSV1K
AC P232I0;
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UNO6_CLOPA
ID UNO6_CLO]
AC P81351;
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Krishna R.G., Chin C.C.Q., Wold F.;
Krishna R.G., Chin C.C.Q., Wold F.;
N'-terminal sequence analysis of N alpha-acetylated proteins after
unblocking with N-acylaminoacyl-peptide hydrolase.";
Anal. Blochem. 199:45-50(1991).
-!- FUNCTION: This enzyme catalyses the hydrolysis of the N-terminal
peptide bond of an N-acetylated peptide to generate an N-acetylated amino acid and a peptide with a free N-terminus. It
preferentially cleaves off Ac-Ala, Ac-Met and Ac-Ser.
-!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)0 = acylamino acid
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Fibroblast,
MEDLINE=9500997; PubMed=7523108;
MEDLINE=9500997; PubMed=7523108;
MEDLINE=9500997; PubMed=7523108;
MEDLINE=9500997; PubMed=7523108;
M. Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 6.6, its MW is: 19 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY.1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-MAR-2004 (Rel. 43, Last amotetation update)
Acylamino-acid-releasing enzyme (EC 3.4.19.1) (AARE) (Acyl-peptide hydrolase) (APH) (Acylaminoacyl-peptidase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus,
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                          01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
ID-WAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h Similarity 33.3%; Pred. No. 1.4e+05; 1; Conservative 1; Mismatches 1; Indels
                                                                                    0; Indels
                                           Length 5;
  582 MW; GAAABIBIA6F00000 CRC64;
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                                           Score 7; DB 1; Le
Pred. No. 1.4e+05;
1; Mismatches 0;
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                                             22.6%;
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                       Query Match
Best Local Similarity
1, Conserve
                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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Matches 1; Conserv
      5 AA;
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UF01 MOUSE
ID UF01 MOUSE
AC P38639;
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P25154;
      SEQUENCE
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RESULT 11 ACPH\_RABIT

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Search completed: June 2, 2004, 18:58:23 Job time : 11 secs
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SEQUENCE
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Best Local S:
Matches 1;
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                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license apreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                  promoter controlling the
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Silverstein S., Wagner B.K.;
"Analysis of the herpes simplex virus type 1 promoter controlling the expression of the herpes simplex virus type 1 promoter controlling th J. Virol. 65:769-786(1991).
-!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE EMBEDDED. BINDS DNA.
-!- SIMILARITY: Belongs to the herpesviruses VP19C family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
TISSUB-Larva;
MEDLING-S05539; PubMed-9392829;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
Davey M., Bast P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
-!- SIMILARITY: Belongs to the allatostatin family.
MOD RES
7
AMIDATION.
SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia,
Tortricoidea, Tortricidae, Olethreutinae, Cydia.

NCBI_TaxID=82600,
                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                     EMBL; M57646; AAA45830.1; -.
capsid assembly; Coat protein; DNA-binding.
NON TER
SEQÜENCE 6 AA; 703 MW; 67376451A338F000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Cydiastatin 7
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(Rel. 29, Last sequence update)
(Rel. 30, Last annotation update)
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Matches 1; Conserv
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P35919;
01-JUN-1994 (
01-JUN-1994 (
01-OCT-1994 (
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ALL7_CYDPO
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Matches
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Achatina fulica (Giant African snail).
Eukaryota, Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBI_TaxID=6530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                       TISSUE-Ganglion;

MIDDLINE-32565912,

Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;

WWWmide-1, -2 and -3: novel neuromodulatory peptides isolated from agandia of the African giant snail, Achatina fulica.";

FEBS Lett. 323:104-108 [1993].

-1- PUNCTION: Exhibits modulatory effects on the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.6%; Score 7; DB 1; Length 7; 33.3%; Pred. No. 1.4e+05; Vinnatches 0; Indels
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7 AA; 993 MW; 7362D5B69B041310 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        system. Inhibits activity on a central neuron. PIR; $33245; $33245. Neuropeptide; Amidation.
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Q66205 transmissib P70804 azotobacter O34028 arabidopsis O94023 human adeno Q66113 cherry last O94199 human adeno O49199 human adeno O49199 human adeno O42564 fugu rubrip P83073 bacillus ce O47029 enterobacte P72081 nocardia la O28742 oryctolagus P92214 streptomyce P92214 streptomyce P92214 pordeum vul P92403 lophopyrum P92421 peridictyon P9243 lophopyrum P92421 browns iner P92421 browns iner P92421 browns iner P9240 thinopyrum P92210 agropyron c P92210 agropyron c P92240 thinopyrum P92210 agropyron c P92240 thinopyrum P92210 agropyron c P92240 thinopyrum P92390 heteranhel

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STRAIN=2273-108;

MEDLINE=81059885; PubMed=6254986;

MEDLINE=81059885; PubMed=6254986;

Monitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;

Rasembly of the mitochondrial membrane system: Structure and nucleotide sequence of the gene coding for subunit 1 of yeast vytochrome oxidase.";

J. Biol. Chem. 255:11927-11941(1980).

EMBL; V00694; CAA24066.1;

SO, GO,005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.9%; Score 13; DB 8; Length 7; llarity 100.0%; Pred. No. 1e+06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q95945;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Inside intron 5 (Fragment).
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 1
7 AA; 859 MW; 75B7232362CDC460 CRC64;
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Q66205
Q96283
Q96583
Q96583
Q971Q3
Q971Q3
Q971Q0
Q071Q0
Q0
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P92430
P92221
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P92381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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SEQUENCE
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P82181
  SET WAY THE TENT OF THE TENT O
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P82182 spinacia ol
O89100 borrelia bu
Q8100 borrelia bu
Q81981 ladrocia ol
P82541 spinacia ol
P83530 ladrochoacil
O08433 rattus sp.
P83308 gallus gall
O07354 synechococc
G89112 borrelia bu
Q89114 borrelia bu
Q89104 borrelia bu
Q89104 cenonhabdi
P93233 lycopersico
Q8436 rattus norv
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                                                                                                                                                            2, 2004, 18:48:29 ; Search time 34.5 Seconds (without alignments) 64.018 Million cell updates/sec
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
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P82181
P82182
Q8GL00
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P82541
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P83308
007354
Q8GL04
Q15897
Q7Z1C0
P93233
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Gapop 10.0 , Gapext 0.5
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sp_human:*
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sp_mammal:*
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sp_phage:*
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Match Length
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STRAIN=CA15,
Stevenson B., Miller J.C.,
"Comparative analyses of Borrelia burgdorferi erp genes and their cp32
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Berrenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,

Hoffmann D., Korn K., Selbig J.;

Hoffmann D., Korn K., Selbig J.;

Holiversity and complexity of HIV-1 drug resistance: A bioinformatics approach to predicting phenotype from genotype.";

Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276 (2002).

EMBL; AF347267; AAX32344.1; -.

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SEQÜENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi (Lyme disease spirochete).
Plasmid group cp32-13.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
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                                                                                                                              Length 6;
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                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prophages: conservation amidst diversity."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases EMBL, AY142106; AAN17857.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
PF-50 protein (Fragment).
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Truncated pol protein (Fragment).
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NCBL_TaxID=11676;
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SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;
Ribosomal protein; Chloroplast; rRNA-binding.
NON TER 6 6
SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;
                                                                                                                           Query Match 35.5%; Score 11; DB 10; Best Local Similarity 66.7%; Pred. No. 1e+06; Matches 2; Conservative 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 AA.
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Best Local Similarity 66.7
Matches 2; Conservative
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Q8GL00
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MEDLLIRE=20435798; PubMed=10874046;
MEDLLIRE=20435798; DubMed=10874046;
Yamaquchi K., Subramanian A.R.;
"The plastid ribosomal proteins. Identification of all the proteins in the 50 % subunit of an organelle ribosome (chloroplast).";
J. Biol. Chem. 275:28466-28482(200).
-:- PUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 50s ribosomal protein L10 gamma (Fragment).
Spinacia oleracea (Spinach).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Spinacia.
                                                          01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 508 ribosomal protein L10 beta (Fragment).
Spinacia oleracea (Spinach).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophylales; Amaranthaceae; Spinacia.
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-: SIBCELLIULAR LOCATION: CHLOROPLAST.
-: MISCELLANGOUS. ON THE 2D-GEL ITS MW IS: 16.5 KDA.
-: MISCELLANGOUS. ON THE 2D-GEL ITS MW IS: 16.5 KDA.
-: MILLARITY: BELONGS TO THE LIOP FAMILY OF RIBOSOMAL PROTEINS.
GO; GO:0009507; C:chloroplast; IEA.
GO; GO:0019843; F:rRNA binding; IEA.
GO; GO:0019355; F:structural constituent of ribosome; IEA.
INTERPRO: IPRO02363; Ribosomal LiOeub.
PROSITE; PS01109; RIBOSOMAL_LIO, PARTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AA; 675 MW; 6321B415B05DB000 CRC64;
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            6 AA.
         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                       ALWARO; TISSUE=Leaf;
135798; PubMed=10874046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 2; Conservative
         PRELIMINARY;
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MEDLINE=20435798;
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RESULT 3 P82182

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Gaps

P82541 RESULT 6 P82541

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Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
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                                                              Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
"High pressure effects step-wise altered protein expression in
Lactobacillus sanfranciscensis.";
proteomics 2.765-774(2002).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
PROTEIN IS: 15 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Gunn;
MEDLINE=91282758; PubMed=1840486;
Sato H., Anno S., Kashiwamata S., Koiwai O.;
Sato H., Anno S., Kashiwamata S., Koiwai O.;
"Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";
Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Bilirubin UDP-glucuronosyltransferase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P83308 PRELIMINARY; PRT; 5 AA.
P83308;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2003 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
FMRFamide-like neuropeptide (LFLRF-amide)
Gallus Gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER 1 1 SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;
                                                                                                                                                                                                                                                                                                                                               7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Conservative
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TISSUE=Brain;
PubMed=6137771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LTL 3
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SEQUENCE
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Q08433;
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Q08433
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Spermarophyta, Magnoliophyta, eudicotyledons, core eudicots;
Caryophyllales, Amaranthaceae, Spinacia.
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Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria, Firmicutes, Lactobacillales, Lactobacillus.
Lactobacillus.
                             Score 11; DB 15; Length 7;
Pred. No. 1e+06;
1; Mismatches 0; Indele
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                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT_2000 (TIEMBLRel. 15, Created)
01-OCT_2000 (TIEMBLRel. 15, Last sequence update)
01-OCT_2003 (TIEMBLRel. 25, Last annotation update)
Chloroplast 30S ribosomal protein S19 beta (Fragment).
Chloroplast oleracea (Spinach)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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PROSITE; PS00323; RIBOSOMAL S19; PARTIAL.
Ribosomal protein; Chloroplast; rRNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                         35.5%; 8 illarity 66.7%; E Conservative 1;
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Query Match
Best Local Similarity
'-hes 2; Conserv?
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les 2, Conserv
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STRAIN=DSM 20451;
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3 ITL 5
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SEQUENCE
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STRAIN=93-0107;
Stevenson B., Miller J.C.;
Stevenson B., Miller J.C.;
Comparative analyses of Borrelia burgdorferi erp genes and their cp32
prophages: conservation amidst diversity.";
Submitrad (Aug-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY142103; AAN17848.1;
GQ; GQ;0046821; C:extrachromosomal DNA; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi (Lyme disease spirochete).
Plasmid group cp32-5.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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"Isolation of chromosome-specific genes by reciprocal probing of arrayed DNAs and cosmid libraries.";
Hum. Mol. Genet. 0.0-0(1995).
EMBL; L32077; AAA73687.1; -.
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                                                                                                                                                                                                                                                             0; Indels
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AX142100; AAN17911.1; -. GO; GO:0046821; C:extrachromosomal DNA; IEA. Plaemid.
                                                                                                                                                                                                       Length 7;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PF-50 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 1 7 AA; 914 MW; 6337244330504310 CRC64;
                                                                                                                       1 1 7 AA; 849 MW; 6337244330569ED0 CRC64;
                                                                                                                                                                                                 Query Match 29.0%; Score 9; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches C
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Matches 2; Conserv
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TISSUE=Placenta;
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SEQUENCE
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SEQUENCE
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Q8GL04;
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Q15897;
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Q8GL04
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MEDLINES9231861; PubMed=10217509;
MEDLINES9231861; PubMed=10217509;
Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
"Organization and expression of nitrogen-fixation genes in the aerobic nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stevenson B., Miller J.C., "Comparative analyses of Borrella burgdorferi erp genes and their cp32 prophages: conservation amidst diversity.";
                                                                                                                                                                                                                                                                                                                                                                              Gapa
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Plasmid group cp32-9.
Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothece PCC 8801).
Bacteria; Cyanobacteria; Chrococcales; Cyanothece.
  "A novel active pentapeptide from chicken brain identified by antibodies to FWRRamide";
Nature 305:228-330(1983).
-!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
-!- STATLARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
Neuropeptide; Amidation.
MOD RES
SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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                                                                                                                                                                                                                                                                                                                29.0%; Score 9; DB 13; Length 5; 50.0%; Pred. No. 1e+06; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.0%; Score 9; DB 2; Length 7; 28.6%; Pred. No. 1e+06; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       007354 PRELIMINARY, PRT; 7 AA. 007354; CTEMBLEL 04, Created) 01-UJL-1997 (TrEMBLEL 04, Last sequence update) 01-DBC-2001 (TrEMBLEL 19, Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;
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Microbiology 145:743-753(1999),
March AF003700; AAC35193.1; -.
NON TER 1
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1 ISFDLVR
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Search completed: June
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Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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1e+06;
ches 0; Indels
                                                                   0; Indels
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
11-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
LB-ACSIB.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Bradshaw H., Graves T., Blair T.;
"The sequence of C. elegans cosmid W01B11.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                            29.0%; Score 9; DB 4; Length 7; llarity 100.0%; Pred. No. 1e+06; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson R.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein W01B11.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF043704; AAO38592.1; -.
Hypothetical protein.
SEQUENCE 7 AA; 874 MW; 72D1A9DB5041A6F0 CRC64;
                       7 AA; 814 MW; 672B1DD3372046B0 CRC64;
                                                                                                                                                                          7 AA.
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Pred. No. 1e+0
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed=9851916;
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Similarity 33.3%;
1; Conservative
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Best Local Similarity
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                                          Query Match
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Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-Bristol N2;
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Q7Z1C0
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Upcopersion esculentum (Tomato).

C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Oc Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; oc lamida; Solanales; Solanacea; Solanum.

OX NCBI TaxID=4081;

RN MEDLINE=97351561; PubMed=9207843;

RY Synthase genes by elicitor in suspension cultures of tomato cultures of tomato of the secondary of seven 1-aminocyclopropane-1-carboxylate

RY Synthase genes by elicitor in suspension cultures of tomato

RY Solo (1997).

RN EMBL, U75623; AAA49681;

RN Lyase.

BR GO; GO:0016829; F:1yase activity; IEA.

KW Lyase.

FY NON TER

CO-CO:0016829; F:1yase activity; IEA.

RW Lyase.

CO-CO:0016829; F:1yase activity; IEA.

CO-CO:0016829; F:1yase activity; IEA.

RN Lyase.

CO-CO:0016829; F:1yase activity; IEA.

RN Lyase.

FY NON TER

CO-CO:0016829; F:1yase activity; IEA.

FY NON TER

Best Local Similarity 100.0%; Pred. No. 1e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps (1)

CO-CO:0016829; F:1yase activity (1)

CO-CO:0016829; F:1yase activ
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2, 2004, 18:47:08 ; Search time 49 Seconds (without alignments) 40.364 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 7
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Perfect score:
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Maximum DB
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geneseqp19808:\* geneseqp20008:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2002s:\* geneseqp2003bs:\* geneseqp2003bs:\*

A\_Geneseq\_29Jan04:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SYNAGIS a Haemagglu DPI trypt Schizophr Human API Human RSV Rheumatoi Rheumatoi Depressio Schizophr Multiple Multiple Respirato Breast ca SYNAGIS a Nucleotid Abp66518 Human RSV Alzheimer . cerevi Vascular Vascular Prostate Description Aay42013 F Aay41889 F Abb55870 Abb56283 Abb56281 Abb56281 Abb56981 Abb26981 Aau2669 Aau2649 Bau2649 Bau2649 Bab52355 Abb56010 Bab56010 Bab56010 Bab59042 Abb56010 Bab59042 Abb59042 Abb59042 Aaw82668 Aaw82668 Aaw69269 Aab02931 ABB56283 ABB55981 AAU28602 AAB02931 Length Query Score Result No.

Aae10492 Humanised	Abp66389 Human RSV	Abp66450 Human RSV	5485 Humar	9796 Zinc	3455 Zinc	2 Zinc	7 Zinc	o zinc	Abb07139 Human ery	Aae28044 Human mod	Abu69348 Respirato	Abu69252 Respirato	m	2 Zinc	임	Zinc (		Ada65573 Zinc fing	Ade35808 SYNAGIS a
4 AAE10492	5 ABP66389	5 ABP66450	5 ABP66485	5 ABP49796	5 ABP48455	5 ABP51172	5 ABP49577	5 ABP49790	5 ABB07139	5 AAE28044	6 ABU69348	6 ABU69252	6 ABU69313	•	7 ADA62425	7 ADA64000	7 ADA65571	7 ADA65573	7 ADE35808
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26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Human, variable heavy domain, variable light domain, CDR; VH; VL; RSV; complementarity determining region; respiratory syncytial virus; virucide; pulmonary; antiinflammatory; cardiant; anti-HTV; vaccine; immunostimulant; gene therapy; costic fibrosis; bone marrow transplant; bronchopulmonary dysplasia; congenital heart disease; congenital immunodeficiency; acquired immunodeficiency. Antibody for treating respiratory syncytial virus (RSV) infection, comprises a variable heavy/light domain or complementarity determining regions 1 - 3 of variable light/heavy chains, that immunospecifically Human RSV antibody VL CDR2 fragment. Johnson LS; ABP66518 standard; peptide; 7 AA. 28-NOV-2001; 2001WO-US044807 28-NOV-2000; 2000US-00724396 28-NOV-2000; 2000US-00724531 (first entry) (MEDI-) MEDIUMMUNE INC. Young JF, Koenig S, oinds to RSV antigen. WPI; 2002-706803/76. WO200243660-A2. Homo sapiens 36-JUN-2002 34-DEC-2002 ABP66518; ABP66518

ILD ABP6

AAC ABP6

XX ABP6

XX ABP6

XX ABP6

XX Huma

XX Huma

XX Homo

Claim 8; Page 55; 298pp; English.

The invention relates to a novel antibody comprising a variable heavy (VH) domain, variable light (VL) domain, VH complementarity determining region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the antibody immunospecifically binds to a respiratory syncytial virus (RSV) antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV, and immunostimulant activity. The polynucleotides of the invention may

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have a use in a vaccine, and in gene therapy. The antibody is useful for treating or ameliorating a RSV infection in a human. The antibody is also useful for preventing, treating or ameliorating one or more symptoms associated with RSV infection in a mammal, e.g. cystic fibrosis, bronchopulmonary dysplasia, congenital heart disease, congenital immunodeficiency, or acquired immunodeficiency, or after a bone marrow transplant. The sequence represents a complementary determining region peptide from a human RSV antibody of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Respiratory syncytial virus; RSV; vaccine; antibody; variable heavy domain; VH; variable light domain; VL; complementarity determining region; CDR; CDR1; CDR2; CDR3; RSV infection; cystic fibrosis; bronchopulmonary dysplasia; congenital heart disease; congenital immunodeficiency; acquired immune deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody comprising a variable heavy (VH) or variable light (VL) domain or complementarity determining region (CDR), such as CDR1, CDR2, or CDR3, useful for preventing or treating a respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes an antibody comprising a variable heavy (VH) or variable light (VL) domain or complementarity determining region (CDR), such as CDR1, CDR2, which immunospecifically binds to a respiratory syncytial virus (RSV) antigen and is not SYNAGIS (RTW). The antibody, pharmaceutical compositions and methods are useful for preventing, treating or ameliorating a RSV infection in patients with cystic fibrosis, bronchopulmonary dysplasia, congenital heart disease, congenital immunodeficiency, or acquired immuno deficiency, or patients having had a bone marrow transplant or the elderly. This is the anino acid sequence of a respiratory syncytial virus (RSV) antibody peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Respiratory syncytial virus (RSV) antibody fragment #126.
                                                                                                                                                                                                                  Score 20; DB 5; Length 7; Pred. No. 1.4e+06; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson LS;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU69381 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 24; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-2001; 2001US-00996288.
                                                                                                                                                                                                                  Similarity 80.0%; 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone marrow transplant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        foung JF, Koenig S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-340947/32.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                              Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU69381;
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ABU69381
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The invention relates to a method of preventing, treating or ameliorating one or more symptoms associated with a respiratory syncytial virus (RSV) infection in a mammal. A sustained release formulation comprising one or more antibodies or their fragments that immunospecifically bind to one or more RSV antigens and a pharmaceutical composition comprising one or more antibodies or their fragments that immunospecifically bind to one or more RSV antigens formulated for pulmonary delivery is useful for preventing, treating or ameliorating one or more symptoms associated with a RSV infection in a mammal by administering the formulation to the mammal, or the composition to the lungs of the mammal. The antibodies bind to RSV antigen with a high affinity and/or high avidity. The methods use lower doses of antibodies which immunospecifically bind to RSV antigen, and which provide a more effective prophylaxis. The present sequence represents the amino acid sequence of a complementarity determining region based on the SYNAGIS antibody.
                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preventing, treating or ameliorating symptoms associated with respiratory syncytial virus infection in mammal by administering antibodies or their fragments that immunospecifically bind to RSV antigens.
                                                                                                                                                                                                                                                                                                                                       respiratory syncytial virus; RSV infection; high affinity antibody; high avidity antibody; low antibody dose; more effective prophylaxis; complementarity determining region; CDR; human.
                                    Gaps
                                                                                                                                                                                                                                                                                                          SYNAGIS antibody based light chain variable region 2, VL2, CDR #54
                                  ;
Score 20; DB 6; Length 7; Pred. No. 1.4e+06; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.5%; Score 20; DB 7; Length 7; 80.0%; Pred. No. 1.4e+06; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 111; SEQ ID NO 164; 161pp; English.
                                                                                                                                                                                                ADE35876 standard; peptide; 7 AA.
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64.5%;
llarity 80.0%;
Conservative
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JOHNSON L S.
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                 Best Local Similarity
Matches 4; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                       29-JAN-2004
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                                                                                                                                                                                                                                     ADE35876;
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KOEN/)
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                                                                                                                                                               RESULT 3
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ઠે d AAY42013 standard; peptide; 7 AA.

AAY42013;

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This sequence represents a fragment of the heavy chain (HAI) of the haemagglutinin of influenza virus. This sequence was used to test the acryloylated peptide polymer of the invention. The peptide polymers are used to raise an immune response to a peptide epitope (such as this sequence), and also as diagnostic tools. Polymers (molecular wt. >600 kDa.) can be prepared with virtually any number of the same or different epitopes by a method that allows purification of the individual determinants, avoids errors inherent in long sequential syntheses in which protected peptide fragments are not used, thus avoiding solubility and purification problems. Multiple copies of many different peptide epitopes may be incorporated into a single polymeric structure to allow utilisation of the range of T cell epitopes required for outbred populations in conjunction with epitopes representing different pathogenic serodemes, thus making them a significant advance in synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acryloylated peptide polymers - useful for synthetic vaccine technology, for raising an immune response to peptide epitope and as diagnostic tool
                                                                                                                                                   Acryloylated peptide polymer; immune response; peptide epitope; synthetic vaccine; enzymatically cleavable site.
                                                                                                                                                                                                                                                                           /note= "linked to acryloylated peptide polymer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19; DB 2; Length 7;
Pred. No. 1.4e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Obrien-Simpson NM, Brown LE, Zeng W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES. (CSIR) COMMONTRALITH SCI & IND RES ORG. (UTME ) UNIV MELBOURNE. (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                    Haemagglutinin heavy chain (HA1) fragment
                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 20; 77pp; English.
              AAW69269 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                  98WO-AU000076
                                                                                                                                                                                                                                                                                                                                                                                                                   97AU-00005071
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Similarity 80.0%;
4; Conservative
                                                                                 29-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Good MF;
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                         Influenza virus.
                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jackson DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brandt ER,
                                                 AAW69269;
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AAW69269
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Ede NJ;

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arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of featuree. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally comprises: (a) analysing a sample of serum or plasma and optionally comprises: (a) analysing a sample of serum or plasma and optionally comprises: (a) analysing a sample of serum or plasma and optionally comprises: (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA, and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature or plasma from one or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy protocols. AAY41131 represent expression reference protein isoform peptides and AAZ25066 to AAZ25068 represent degenerate probes for RPIS, which are all cused in the exemplification of the present invention
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                                                                                                                                 Human, rheumatoid arthritis, RA, diagnosis, RPI, RADF, detection, rheumatoid arthritis diagnostic feature, ERRI, synovial fluid, rheumatoid arthritis diagnostic protein isoform, screening; expression reference protein isoform, prognosis.
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                                                                                           Rheumatoid arthritis diagnostic protein isoform peptide #164.
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4; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                     99WO-GB000763
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                                                        (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          electrophoresis.
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                                                        09-DEC-1999
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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or progneted features and VPI is useful for the screening, diagnosis or prognessis of VD, for determining the stage or the affect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stege of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
                                                                                                                                                   Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.3%; Score 19; DB 4; Length 7; 66.7%; Pred. No. 1.4e+06; ive 1; Mismatches 1; Indels
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                                                                                                  Vascular dementia-associated protein isoform (VPI) 70.
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                                                                                                                                                                                 diagnosis; prognosis; gene therapy
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28-NOV-2000; 2000US-00724391.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                               Homo sapiens.
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                                                 15-FEB-2002
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  ABB55870;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thritis (RA) using two-dimensional electrophoreeis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method compariess: (a) analysing a sample of serum or plasma and optionally compariess: (a) analysing a sample of serum or plasma and optionally dimensional array of features) (b) identifying at least one chosen dimensional array of features of b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature or more persons without RA, where the relative abundance of the chosen feature or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence of absence of RA in the subject. The method can also be used in clinical absence of RA in the subject. The method can also be used in clinical chosen feature in soforms (RPIs), and for production of antibodies to RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy protections and the expression reference protein isoform peptides and AAZ25066 to AAZ25068 represent edgenerate probes for RPIs, which are all cust and the exemplification of the present invention
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                                                                                                                                                                                                 Human, rheumatoid arthritis, RA, diagnosis, RPI, RADF, detection, rheumatoid arthritis diagnostic feature, BRPI, synovial fluid, rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                   Rheumatoid arthritis diagnostic protein isoform peptide #40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 2; Length 7; Pred. No. 1.4e+06; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
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AAY41889 standard; peptide; 7 AA
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                                                                                                  (first entry)
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Best Local Similarity 66.7
Matches 4; Conservative
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2 TFELSR 7
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Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;

diagnosis; prognosis; gene therapy,

ABB55870 standard; peptide; 7 AA.

ABB55870 ID ABB5 XX RESULT 7

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20-SEP-2001

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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject comprising analysing body fluid from the features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSP) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
                                                                                                                                                                                                   useful for
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                                                                                                                                                                                                 Screening, diagnosis or prognosis of vascular dementia (VD), useful determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
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66.7%; Pred. No. 1.4e+06;
iive 1; Mismatches 1;
                                                                   (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
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                                                                                                            Parekh RB, Rohlff C;
                                                                                                                                                                                                                                                                                                                     Claim 6; Page 33; 151pp; English.
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08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
24-NOV-2000; 2000GB-00028734
28-NOV-2000; 2000US-00724391
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                                                                                                                 Herath HMAC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD. for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                         Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 40; 151pp; English
                                                                                                                                                                             15-MAR-2000; 2000GB-00006285.
24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
                                                                                                                                    14-MAR-2001; 2001WO-GB001106
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Best Local Similarity
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TFELSR
                                             WO200169261-A2.
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    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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15-FEB-2002

Vascular

ABB55981;

RESULT 9 ABB55981

Best Loc Matches

ਨੇ 셤 20-SEP-2001

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schizophrenia. The sequences can be used for treatment and diagnosis of
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                                                                                                  The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest peptides of these proteins. Some of the DPIs (AMU28404-AMU28625) described are decreased in the carebrospinal fluid (CSF) of BAD (bipolar affective disorder) subjects, whilst other DPIS (AAU28626-AAU28887) are increased in BAD subjects, Also described are peptide sequences identified from DPI-45 and DPI-31 and the nucleic acid sequence they are encoded by. The sequences of the invention are useful for clinical neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder, BP), maniac-depressive illnesses, attention deficit disorders, achizoaffective disorders, and unipolar affective disorders. The present increase represents one of the DPI tryptic disest peptides of the present
                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New schizophrenta associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizophrenia-associated protein isoform, SPI, SPI-206; SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of
                        Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.
                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizophrenia-Associated Protein Isoform (SPI) peptide #198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rohlff C, Terrett JA, Tyson KL;
                                                                                                                                                                                                                                                                                                                                   61.3%; Score 19; DB 4; Length 7;
.larity 66.7%; Pred. No. 1.4e+06;
Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OXFO-) OXFORD GLYCOSCIENCES UK LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 32; 148pp; English.
                                                                            Disclosure; Page 34; 153pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU24969 standard; peptide; 7 AA.
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28-DEC-2000; 2000US-00750395.
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WPI; 2001-570626/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-570624/64.
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
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2 TFELSR 7
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                                                                                                                                                                                                                                                                                                         Sequence 7 AA;
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The invention relates to a preparation comprising an isolated Bipolar Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are used to screen, diagnose or prognose of BAD or unipolar depression, dentify a cubject at risk of developing BAD or unipolar depression, identify a cubject at risk of developing BAD or unipolar depression, identify a cubject at risk of developing BAD or unipolar depression, or monitor the effect of therapy in a subject. They are also used to screen for or identify agents that interact with a DPI. These agents, antibodies against the DPIs, and nucleic acids encoding the DPIs are used to treat or prevent BAD or unipolar depression. Diseases that can be treated are unipolar affective disorder, a schizoaffective disorder, a bipolar or proteomic approach of using DPIs for screening, diagnosis or prognosis of unipolar depression overcomes the problems of using gene control of using DPIs for screening, diagnosis or prognosis of EAD or unipolar depression overcomes the problems of using gene companysis, such as not being able to obtain central nervous system (CMS) tissue from a living patient under normal circumstances. The present sequence is a DIP decreased in the CSF (cerebro-spinal fluid) of
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schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as another acid probe to detect the presence of nucleic acids or SPIs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, Bipolar Affective Disorder, BAD, Depression-Associated feature, DF; Depression-Associated protein isoform, DPI, Cerebro-spinal fluid, CSF; antidepressant, antimanic, nootropic, tranquillser, neuroleptic, attention deficient disorder, schizoaffective disorder; unipolar affective disorder.
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                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                           Score 19; DB 4; I
Pred. No. 1.4e+06;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Depression-Associated Protein isoform DPI-208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU26249 standard; peptide; 7 AA.
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08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
                                                                                                                                                                                                                                                                       61.3%;
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                                                                                                                                                                                                                                                                                                                                                4; Conservative
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                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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TFELSR
                                                                                                                                                                                                                                                                                                                                                                                                                         2 TLKLSR
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                                                                                                                                                                                          Sequence 7 AA;
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AAU26249
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The invention relates to methods for the screening, diagnosis and prognosis of Alzheimer's disease. The methods involve the detection of Alzheimer's Disease-Associated Peatures (AFS) and Alzheimer's Disease-Associated Peatures (AFS) and Alzheimer's Disease-Associated Protein Isoforms (APIS) in cerebrospinal fluid, serum or Baptsma. The abundance of the AFS and APIS is then normalised to an Baptsmession Reference Protein Isoform (BRRI) in order to determine whether a patient is suffering from, or has a predisposition to, Alzheimer's Beaverity of Alzheimer's Disease. The relative abundance of the AFS and APIS correlates with the produced from an API by proteolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening for Alzheimer's disease in a mammal, by making two-dimensional array of a feature whose relative abundance correlates with disease, and comparing with abundance of the feature in samples of healthy persons.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, neuroprotective, nootropic, gene therapy; vaccine,
Alzhiemer's disease, Alzheimer's Disease-Associated Feature, AF;
Alzheimer's Disease-Associated Frotein Isoform; API; tryptic digest;
Axpression Reference Protein Isoform; ERPI; proteolysis.
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Rohlff C, Silber BM, Stiger TR, Sunderland PT;
, White F, Williams SA;
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Pred. No. 1.4e+06;
1; Mismatches 1; Indels
                                           Length 7;
                        Score 19; DB 4; Len
Pred. No. 1.4e+06;
                                                                                    1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Human API-125 tryptic digest peptide #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OXFO-) OXFORD GLYCOSCIENCES UK LTD. (PFIZ ) PFIZER INC.
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                                                                                                                                                                                                                                                                                            ABB52355 standard; peptide; 7 AA.
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Best Local Similarity 66.7%;
Matches 4; Conservative
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                                             Query Match 61.3
Best Local Similarity 66.7
Matches 4; Conservative
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2 TFELSR 7
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Sequence 7 AA;
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28-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                         ABB52355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to methods and compositions for screening, diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) Associated Features (SPS) and SCH. Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, studying the effectiveness of treatments and for identifying potential therapeutic agents. The method is used for (1) screening or diagnosis of SCH and the relative abundance of at least 1 chosen feature correlates with the presence or absence of SCH; and (2) monitoring the effect of the herapy administered to a subject with SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The secondary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectivenes of treatment and as targets to identify and produce potential therapeutic agents for the treatment of SCH. The paucity of detectable neuralgic defects distinguishes neuropsychiatric disorders such as SCH from neurological disorders, where manifestations of antomical and biochemical changes have been identified in many cases. Consequently the identification and characterisation of cellular and/or molecular causative defects and neuropathies are necessary for improved treatment of neuropsychiatric disorders. Abuls114-ANUS762 represent the amino acid sequences of schizophrenia-associated isoforms used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing and monitoring Schizophrenia by detecting the presence of Schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid.
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizophrenia, neuroleptic; diagnostic; neuropsychiatric disorder; neurological disorder; neuropathy.
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                                                                                                                                      1; Indels
                                                                                         Score 19; DB 4; Length 7; Pred. No. 1.4e+06; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizophrenia-associated isoform peptide #198.
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                                                                                                                                                                                                                                                                                                                                            AAU15313 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000GB-00004415
2000US-00750395
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                                                                                         61.3%;
ilarity 66.7%;
Conservative
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    subjects having BAD
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                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                    2 TLKLSR 7
                                                                                                                                                                                                               TFELSR
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                                                Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-FEB-2000;
28-DEC-2000;
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The invention relates to a novel antibody comprising a variable heavy

(WH) domain, variable light (WL) domain, WH complementarity determining
region (CDR1, "WH CDR2, "WH CDR1, "WL CDR2, "WL CDR3, where the
antibody immunospecifically binds to a respiratory syncytial virus (RSV)
antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
invention has varicale, pullmonary, antihifflammatory, cardiant, anti-HIV,
and immunostimulant activity. The polymuleotides of the invention may
have a use in a vaccine, and in gene therapy. The antibody is useful for
treating or ameliorating a RSV infection in a human. The antibody is also
useful for preventing, treating or ameliorating one or more symptoms
associated with RSV infection in a mammal, e.g. cystic fibrosis,
conchopulmonary dysplasia, congenital heart disease, congenital
immunodeficiency or acquired immunodeficiency, or after a bone marrow
transplant. The sequence represents a complementary determining region
peptide from a human RSV antibody of the invention
                                                                                                                                                                                               Human, variable heavy domain, variable light domain, CDR, VH, VL, RSV, complementarity determining region, respiratory syncytial virus; virucide, pulmonary, antiinflammatory, cardiant, anti-HIV; vaccine; immunostimulant, gene therapy, cystic fibrosis; bone marrow transplant, bronchopulmonary dysplasia; congenital heart disease; congenital immunodeficiency; acquired immunodeficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody for treating respiratory syncytial virus (RSV) infection, comprises a variable heavy/light domain or complementarity determining regions 1 - 3 of variable light/heavy chains, that immunospecifically binds to RSV antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.3%; Score 19; DB 5; Length 7; 80.0%; Pred. No. 1.4e+06; ive 1; Mismatches 0; Indels
                                                                                                                                                              Human RSV antibody VL CDR2 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Page 55; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Young JF, Koenig S, Johnson LS;
                                       ABP66489 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-2001; 2001WO-US044807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-2000; 2000US-00724396.
28-NOV-2000; 2000US-00724531.
                                                                                                                    (first entry)
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                               ABP66489;
RESULT 15
ABP66489
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Search completed: June 2, 2004, 18:57:51 Job time : 50 secs

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Gaps . 0

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Sequence 164, Application US/0996288

Patent No. US20020177126A1

Patent No. US20020177126A1

APPLICANT: Young, James

APPLICANT: Scott, Koenig

APPLICANT: Leslie, Johnson

TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophyl

TITLE OF INVENTION: and Treatment

FILE REPERROE: 10271-047-999

CURRENT APPLICATION NUMBER: US/09/996,288

CURRENT PILING DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 259

SOFTWARE: PatentIn version 3.1
  Sequence 396, App
Sequence 353, Ap
Sequence 354, Ap
Sequence 354, Ap
Sequence 20, Appl
Sequence 21, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 354, App
Sequence 354, Ap
Sequence 354, Appl
Sequence 353, Appl
Sequence 354, Appl
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US-09-989-789-1396
US-09-989-789-1391
US-09-989-789-1391
US-09-989-789-1391
US-09-989-789-13544
US-09-989-789-13544
US-09-986-288-131
US-09-996-288-131
US-09-998-994-1354
US-10-084-388-335
US-10-084-383-335
US-10-481-883-335
US-10-481-883-335
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Publication No. US20030091584A1
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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US-09-996-265-164
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US-09-996-288-164
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US-09-996-288-164
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Sequence 164, App
Sequence 164, App
Sequence 198, App
Sequence 7, Appli
Sequence 135, App
Sequence 145, App
Sequence 145, App
Sequence 145, App
Sequence 135, Appl
Sequence 135, Appl
Sequence 240, Appl
                                                                                                                                          2, 2004, 18:59:52 ; Search time 37.5 Seconds (without alignments) 52.517 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCCMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_TBW FUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/SCT_NBW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NBW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO7_NBW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NBW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCCMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCCMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCCMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCCMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCCMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCCMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCCMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCCMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCCMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCCMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCCMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCCMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCCMB.pep:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-996-288-164

US-09-996-288-164

US-09-998-198

US-09-998-370

US-09-998-370

US-09-998-370

US-09-998-370

US-09-998-389-145

US-09-996-288-135

US-09-996-288-135

US-09-996-288-135

US-09-996-288-135

US-10-601-100-105

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Maximum Match 100%
Listing first 45 summaries
                                                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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                                                                                                                                                 Run on:
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APPLICANT: Williams, Stephen A.

APPLICANT: Williams, Stephen A.

TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and

TITLE OF INVENTION: Nacleic Acid Molecules, Polypeptides and Treatment of TITLE OF INVENTION: Alzheimer's Disease

TITLE OF INVENTION: Alzheimer's Disease

FILE REFERENCE: 2572-1-001 N2

CURRENT APPLICATION NUMBER: US 60/194,504

PRIOR APPLICATION NUMBER: US 60/194,504

PRIOR PILING DATE: 2000-04-03

PRIOR PILING DATE: 2000-01-128

NUMBER OF SEQ ID NOS: 492

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 370

LENGTH: 7
                                                                         Gaps
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Sequence 77, Application US/0998909

Patent No. US20020164664A1

GENERAL INFORMATION:

APPLICANT: Hlavaty, John

TILE OF INVENTION: Detection and Treatment of Prostate Cancer

TILE OF INVENTION: Detection and Treatment of Prostate Cancer

FILE REFERENCE: 12007

CURRENT APPLICATION NUMBER: US/09/998,909

CURRENT FILING DATE: 2001-11-30

PRIOR FILING DATE: 2000-11-30

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.0
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Patent No. US20020164668A1

GENERAL INFORMATION:

APPLICANT: Durham, L.Kathryn

APPLICANT: Friedman, David L.

APPLICANT: Friedman, David L.

APPLICANT: Friedman, David M.

APPLICANT: Parekh, Rajesh Bhikhu

APPLICANT: Porter, David M.

APPLICANT: Rohlff, Christian

APPLICANT: Thomas R.

APPLICANT: Stiger, Thomas R.

APPLICANT: Sunderland, P. Trey

APPLICANT: Sunderland, P. Trey

APPLICANT: Sunderland, P. Trey

APPLICANT: Gunderland, P. Trey

APPLICANT: Gunderland, P. Trey

APPLICANT: Males
                                                                       1; Indels
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1e+06;
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                                Length 7;
                             Score 19; DB 9;
Pred. No. 1e+06;
1; Mismatches
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Pred. No.
                           61.3%;
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                       Conservative
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ORGANISM: Homo Bapiens
US-09-998-909-7
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                             Query Match
Best Local Similarity
Matches 4; Conserv
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2 TPELSR 7
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US-09-826-290-370
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APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-048-999
CURRENT APPLICATION NUMBER: 105/09/996,265
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
SEQ ID NO 164
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Oliver, Cynthia
APPLICANT: Allan, Christian
APPLICANT: Allan, Christian
APPLICANT: Chang, Stephen
ITLE CAMP: Chang, Stephen
ITLE OF INVENTION: STEPHEN ANTI-RESPIRATORY SYNCYTIAL VIRUS (RSV) ANTIBODY FORMUL
FILE REPERENCE: 10271-071-999
CURRENT APPLICATION NUMBER: US/10/461,863
CURRENT PILING DATE: 2003-06-13
PRIOR PILING DATE: 2002-06-14
NUMBER: OF SEQ ID NOS: 209
SEQ ID NOS: 209
SEQ ID NO 164
LENGTH: 7
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Patent No. US20020142303A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Parekh, Rajesh
TITLE OF INVENTION: SCHIZOPHRENIA
FILE REFERENCE: 9195-061-999-061-999-0791,378
CURRENT APPLICATION NUMBER: US/09/791,378
PRIOR PILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 677
SOFTWARE: Patentin version 3.0
SEQ ID NO 198
LENGTH: 7
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Pred. No. 1e+06;
1; Mismatches 0; Indels
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Sequence 164, Application US/10461863
Publication No. US20040018200A1
GENERAL INFORMATION:
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80.0%;
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80.0%;
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CRGANISM: Homo sapiens
US-09-791-378-198
                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Homo sapiens
US-09-996-265-164
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US-10-461-863-164
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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US-09-191-389-145

US-09-191-389-145

US-09-191-389-145

Sequence 145. Application US/09791389

Publication No. US20030032773A1

GENERAL INFORMATION:
APPLICANT: Perseth, Rejeeh Bhikhu
APPLICANT: Perseth, Rejeeh Bhikhu
APPLICANT: Terrett, Jonathan Alexander
APPLICANT: Terrett, Jonathan Alexander
APPLICANT: Terrett, Jonathan Alexander
APPLICANT: Terrett, Jonathan Alexander
APPLICANT: Tyson, Kerry Louise
TITLE OF INVENTION: Proteins, Genes and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: and Unipolar Depression
FILE REFERENCE: 2543-1-001 N2

FILE REFERENCE: 2543-1-001 N2

CURRENT FILING DATE: 2000-12-24

PRIOR FILING DATE: 2000-12-08

PRIOR FILING DATE: 2000-12-12

PRIOR FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 308

SEQ ID NO 145

LENGTH: 7
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Publication No. US20030091584A1
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: and Treatment
FILE OF INVENTION: and Treatment
FILE OF INVENTION and Treatment
FILE OF INVENTION WHERE: US/09/996,265
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin Version 3.1
SEQ ID NO 135
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Pred. No. 1e+06;
1; Mismatches 0
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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US-09-996-265-135
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US-09-791-389-145
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2 TFELSR 7
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Batent No. US20020177126A1

Batent No. US20020177126A1

BAPLICANT: Young, James

APPLICANT: Scott, Koenig

APPLICANT: Scott, Koenig

TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi

TITLE OF INVENTION: And Treatment

TITLE OF INVENTION: And Treatment

TITLE OF PROPERIOR: 10271-047-999

CURRENT APPLICATION NUMBER: US/09/996,288

UNRENT FILING DATE: 2001-11-28

NUMBER: OF SEQ ID NOS: 259

SOFTWARE: PatentIn version 3.1

SEQ ID NO 135
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                                                    Score 19; DB 9; Length 7; Pred. No. 1e+06; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 9; Length 7; Pred. No. 1e+06; 0; Indels 1; Mismatches 0; Indels
                                                        61.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.3%;
80.0%;
                                                    Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-09-996-288-135
; ORGANISM: homo sapien
US-09-826-290-370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-145
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Best Local Similarity
Matches 4; Conserva
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2 TFELSR 7
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Sequence 135, Application US/10461863
Publication No. US20040018200A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL APPLICANT:
APPLICANT:
APPLICANT:
CHANG, STEABILIZED ANTI-RESPIRATORY SYNCYTIAL VIRUS (RSV) ANTIBODY FORM TITLE OF INVENTION: STABILIZED ANTI-RESPIRATORY SYNCYTIAL VIRUS (RSV) ANTIBODY FORM TITLE OF INVENTION NUMBER: US/10/461,863
CURRENT APPLICATION NUMBER: US/10/461,863
CURRENT FILING DATE: 2003-06-14
NUMBER OF SEQ ID NOS: 209
SOPTHAND PATENTION OF SEQ ID NOS: 209
SOPTHAND PATENTION OF SEQ ID NOS: 209
LENGTH: 7
LENGTH: 
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US-10-264-309-460

IGANIZATION NO. US2004002294A1

SEQUENCE 46.0

PUBLICATION NO. US2004002294A1

GENERAL INPORTATION

APPLICANT: PURHAM, L. KATHEYN

APPLICANT: FRIEDMAN, DAVID L.

APPLICANT: RIBEATH, HERATH

APPLICANT: RAMER, LIDA H.

APPLICANT: RAMER, LIDA H.

APPLICANT: ROHLFF, CHRISTIAN

APPLICANT: SOLIEF, BANICHAEL

APPLICANT: SYDER, PETER J.

APPLICANT: SYDER, PETER J.

APPLICANT: SYDER, PETER J.

APPLICANT: SYDER, PETER J.

APPLICANT: SYDER, ROHEF, CAID MOLECULES, POLYPEPTIDES AND USES THEREFOR, TITLE OF INVENTION: INCLEASE AND TREATMENT OF ALZHEIMER'S DISEASE

TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMER'S DISEASE

TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMER'S DISEASE

TITLE REPRESENCE: DOA-002.01

CURRENT FILING DATE: 2002-10-03

NUMBER OF SEQ ID NOS: 491

SEQ ID NOS: 491

LENGRENT FILING DATE: 2001-10-03

NUMBER OF SEQ ID NOS: 491

LENGRENT FILING DATE: 2001-10-03

NUMBER OF SEQ ID NOS: 491

LENGRENT FILING DATE: 2001-10-03

NUMBER OF SEQ ID NOS: 491

LENGRENT FILING DATE: 2001-10-03

NUMBER OF SEQ ID NOS: 491

LENGRENT FILING DATE: 2001-10-03

NUMBER OF SEQ ID NOS: 491

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NUMBER OF SEQ ID NOS: 491

LENGRENT FILING DATE: 2001-10-03

NUMBER OF SEQ ID NOS: 491

LENGRENT FILING DATE: 2001-10-03

NUMBER OF SEQ ID NOS: 491

LENGRENT FILING DATE: 2001-10-03

NUMBER OF SEQ ID NOS: 491

LENGRENT FILING DATE: 2001-10-03
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Best Local Similarity 66.73
Matches 4, Conservative
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; ORGANISM: Homo sapiens
US-10-264-309-460
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US-10-461-863-135
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2 TFELSR 7
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                                                                                                                                                         Sequence 105, Application US/10601100

publication No. US20040072261A1

publication No. US20040072261A1

publication No. US20040072261A1

GENERAL INFORMATION:

APPLICANT; INNOGENETICS N V.

TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of

TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of

TITLE OF INVENTION: Method for Lee Diagnosis of

CURRENT PILING DATE: 2003-66-20

CURRENT APPLICATION NUMBER: US/10/601,100

PRIOR APPLICATION NUMBER: US 60/396,437

PRIOR PILING DATE: 2002-06-21

PRIOR FILING DATE: 2002-07-17

NUMBER OF SEQ ID NOS: 113

SOFTWARE: Patentin version 3.2

LENGTH: 7

LENGTH: 7
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US-10-044-034-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.3%; Score 19; DB 13; Length 7; Best Local Similarity 80.0%; Pred. No. 1e+06; Matches 4; Conservative 1; Mismatches 0; Indels
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Publication No. US20020169264A1
GENERAL INFORMATION:
APPLICANT: O'BRIEN-SIMPSON, NEIL M.
APPLICANT: EDG. NICHOLAS J.
APPLICANT: EDG. NICHOLAS J.
APPLICANT: BRANDT, EVELYN R.
APPLICANT: BRANDT, EVELYN R.
TITLE OF INVENTION: POLYMERS INCORPORTING PEPTIDES
FILE REFRERENCE: FBRC:006
CURRENT APPLICATION NUMBER: US/10/044,034
CURRENT APPLICATION NUMBER: US/10/044,034
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICANTON NUMBER: P05071
PRIOR FILING DATE: 1997-02-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: homo sapiens
US-10-601-100-105
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2 TFELSR 7
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RESULT 13 US-10-461-863-135

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Gaps

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RESULT 15

US-09-897-107-24

Sequence 24, Application US/09897107

Patent No. US20020137094A1

GENERAL INFORMATION:
TYPLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HAVING TITLE OF INVENTION: THERMOSTABILITY INPROVED BY THE METHOD AND NUCLEIC ACIDS ENCODIN FILE REPRENCE: 2101-07-03

CURRENT APPLICATION NUMBER: UP2000-201920

PRIOR PILING DATE: 2001-07-03

PRIOR PILING DATE: 2001-07-04

PRIOR PILING DATE: 2001-05-31

PRIOR PILING DATE: 2001-05-31

NUMBER OF SEQ ID NOS: 104

SEQ ID NOS: 104

SOFTWARE: Patentin version 3.1

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LENGIN SACCHAROMENE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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Search completed: June 2, 2004, 19:08:55 Job time: 38.5 secs